

1 50

EG327	MNKIYRIIWN SALNAWWAVS ELTRNHTKRA SATVATAVIA TLLFATVQAS.
BZ198	MNKIYRIIWN SALNAWWVS ELTRNHTKRA SATVATAVIA TLLFATVQAN
BZ10	MNKISRIIWN SALNAWWVS ELTRNHTKRA SATVATAVIA TLLFATVQAN
H15	MNKIYRIIWN SALNAWWVS ELTRNHTKRA SATVATAVIA TLLFATVQAN
EG329	MNEILRIIWN SALNAWWVS ELTRNHTKRA SATVKTAVIA TLLFATVQAS
PMC21	MNKIYRIIWN SALNAWWVS ELTRNHTKRA SATVKTAVIA TLLFATVQAS
H38	MNKIYRIIWN SALNAWWAVS ELTRNHTKRA SATVKTAVIA TLLFATVQAN
P20	MNKIYRIIWN SALNAWWVS ELTRNHTKRA SATVATAVIA TLLSATVQAN
Z2491	MNKIYRIIWN SALNAWWAVS ELTRNHTKRA SATVKTAVIA TLLFATVQAN
H41	MNKIYRIIWN SALNAWWAVS ELTRNHTKRA SATVKTAVIA TLLFATVQAN
Consensus	<u>MN-I-R-IWN SALNAWW-VS ELTRNHTKRA SATV-TAVIA TLL-ATVOA-</u>

C1

51 100

EG327	TTDDD...DL YLEPVQRTAV VLSFRSDKEG TGEKE.VTED SNWGVYFDKK
BZ198	ATDDD...DL YLEPVQRTAV VLSFRSDKEG TGEKE.GTED SNWAVYFDEK
BZ10	ATDDD...DL YLEPVQRTAV VLSFRSDKEG TGEKE.GTED SNWAVYFDEK
H15	ATDDD...DL YLEPVQRTAV VLSFRSDKEG TGEKE.GTED SNWAVYFDEK
EG329	ANNEEQEEDL YLDPVLRTVA VLIVNSDKEG TGEKEKVEEN SDWAVYFNEK
PMC21	ANNEEQEEDL YLDPVQRTVA VLIVNSDKEG TGEKEKVEEN SDWAVYFNEK
H38	ATDED..EEE ELEPVVRSAL VLQFMIDKEG NGENE. STGN IGWSIYYDNH
P20	ATDTD..EDE ELESVARSA VLQFMIDKEG NGEIESTGDI GWISIYYDDHN
Z2491	ATDED..EEE ELESVQR.SV VGSIQASMEG SGELET...I SLSMTNDSKE
H41	ATDED..EEE ELESVQR.SV VGSIQASMEG SVELET...I SLSMTNDSKE
Consensus	<u>----- L--V-R-- V----- EG --E-E-----</u>

V1

101 150

EG327	GVLTAGTITL KAGDNLKIKQ NTNENTNASS ... FTYSLK KDLTDLTSVG
BZ198	RVLKAGAITL KAGDNLKIKQ NTNENTNDSS ... FTYSLK KDLTDLTSVE
BZ10	RVLKAGAITL KAGDNLKIKQ NTNENTNENT NDSSFTYSLK KDLTDLTSVE
H15	RVLKAGAITL KAGDNLKIKQ NTNENTNENT NDSSFTYSLK KDLTDLTSVE
EG329	GVLTAIREITL KAGDNLKIKQ NG...TN... ... FTYSLK KDLTDLTSVG
PMC21	GVLTAIREITL KAGDNLKIKQ NG...TN... ... FTYSLK KDLTDLTSVG
H38	NTLHGATVTL KAGDNLKIKQ NTNKNENT NDSSFTYSLK KDLTDLTSVE
P20	TLHG.ATVTL KAGDNLKIKQ SGKD. FTYSLK KELKDLTSVE
Z2491	FVDPTYVVTL KAGDNLKIKQ NTNENTNASS ... FTYSLK KDLTGLINVE
H41	FVDPTYVVTL KAGDNLKIKQ NTNENTNASS ... FTYSLK KDLTGLINVE
Consensus	<u>----- TL KAGDNLKIKQ ----- FTYSLIK K-L--L--V-</u>

V1 C2 V2 C3

151 200

EG327	TEKLSFSANS NKVNITSDTK GLNFAKKTAE TNGDTTVHLN GIGSTLTDTL
BZ198	TEKLSFGANG NKVNITSDTK GLNFAKETAG TNGDPTVHLN GIGSTLTDTL
BZ10	TEKLSFGANG NKVNITSDTK GLNFAKETAG TNGDPTVHLN GIGSTLTDTL
H15	TEKLSFGANG NKVNITSDTK GLNFAKETAG TNGDPTVHLN GIGSTLTDTL
EG329	TEKLSFSANG NKVNITSDTK GLNFAKETAG TNGDTTVHLN GIGSTLTDTL
PMC21	TEKLSFSANG NKVNITSDTK GLNFAKETAG TNGDTTVHLN GIGSTLTDTL
H38	TEKLSFGANG NKVNITSDTK GLNFAKETAG TNGDTTVHLN GIGSTLTDTL
P20	TEKLSFGANG NKVNITSDTK GLNFAKETAG TNGDPTVHLN GIGSTLTDTL
Z2491	TEKLSFGANG KKVNIIISDTK GLNFAKETAG TNGDTTVHLN GIGSTLTDTL
H41	TEKLSFGANG KKVNIIISDTK GLNFAKETAG TNGDTTVHLN GIGSTLTDML
Consensus	<u>TEKLSF-AN- -KVNI-SDTK GLNFAK-TA- TNGD-TVHLN GIGSTLTD-L</u>

C3

FIG. 1

201 250

EG327	LNTGATTNVT	NDNVTDEKK	RAASVKDVLN	AGWNIKGVKP	GTTAS.. DNV
BZ198	LNTGATTNVT	NDNVTDEKK	RAASVKDVLN	AGWNIKGVKP	GTTAS.. DNV
BZ10	LNTGATTNVT	NDNVTDEKK	RAASVKDVLN	AGWNIKGVKP	GTTAS.. DNV
H15	LNTGATTNVT	NDNVTDEKK	RAASVKDVLN	AGWNIKGVKP	GTTAS.. DNV
EG329	LNTGATTNVT	NDNVTDEKK	RAASVKDVLN	AGWNIKGVKP	GTTAS.. DNV
PMC21	LNTGATTNVT	NDNVTDEKK	RAASVKDVLN	AGWNIKGVKP	GTTAS.. DNV
H38	LNTGATTNVT	NDNVTDDKK	RAASVKDVLN	AGWNIKGVKP	GTTAS.. DNV
P20	AGSSASHVDA	GNQST.. HYT	RAASIKDVLN	AGWNIKGVKT	GSTTGQSENV
Z2491	AGSSASHVDA	GNQST.. HYT	RAASIKDVLN	AGWNIKGVKT	GSTTGQSENV
H41	LNTGATTNVT	NDNVTDEKK	RAASVKDVLN	AGWNIKGVKP	GTTAS.. DNV
Consensus	-----A-----	-----T-----	RAAS-KDVLN	AGWNIKGVK-	G-T-----NV

V3 C4 V4

251 300

EG327	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK	RTEVKIGAKT	SVIKEKDGL
BZ198	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK	KTEVKIGAKT	SVIKEKDGL
BZ10	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK	RTEVKIGAKT	SVIKEKDGL
H15	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK	KTEVKIGAKT	SVIKEKDGL
EG329	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK	KTEVKIGAKT	SVIKEKDGL
PMC21	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK	KTEVKIGAKT	SVIKEKDGL
H38	DFVHTYDTVE	FLSADTKTTT	VNVESKDNGK	RTEVKIGAKT	SVIKEKDGL
P20	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK	RTEVKIGAKT	SVIKEKDGL
Z2491	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK	RTEVKIGAKT	SVIKEKDGL
H41	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK	KTEVKIGAKT	SVIKEKDGL
Consensus	DFV-TYDTVE	FLSADTKTTT	VNVESKDNGK	-TEVKIGAKT	SVIKEKDGL

C5

301 350

EG327	VTGKDKGEND	SSTDKGEGLV	TAKEVIDAVN	KAGWRMKTTT	ANGQTGQADK
BZ198	VTGKGKDENG	SSTDEGEGLV	TAKEVIDAVN	KAGWRMKTTT	ANGQTGQADK
BZ10	VTGKGKGENG	SSTDEGEGLV	TAKEVIDAVN	KAGWRMKTTT	ANGQTGQADK
H15	VTGKGKDENG	SSTDEGEGLV	TAKEVIDAVN	KAGWRMKTTT	ANGQTGQADK
EG329	VTGKDKGENG	SSTDEGEGLV	TAKEVIDAVN	KAGWRMKTTT	ANGQTGQADK
PMC21	VTGKDKGENG	SSTDEGEGLV	TAKEVIDAVN	KAGWRMKTTT	ANGQTGQADK
H38	VTGKGKGENG	SSTDEGEGLV	TAKEVIDAVN	KAGWRMKTTT	ANGQTGQADK
P20	VTGKGKGENG	SSTDEGEGLV	TAKEVIDAVN	KAGWRMKTTT	ANGQTGQADK
Z2491	VTGKGKGENG	SSTDEGEGLV	TAKEVIDAVN	KAGWRMKTTT	ANGQTGQADK
H41	VTGKGKGENG	SSTDEGEGLV	TAKEVIDAVN	KAGWRMKTTT	ANGQTGQADK
Consensus	VTGK-K-EN-	SSTD-GEGLV	TAKEVIDAVN	KAGWRMKTTT	ANGQTGQADK

C5

351 400

EG327	FETVTSGTNV	TFASGKGTTA	TVSKDDQGNI	TVMYDVNVGD	ALNVNQLQNS
BZ198	FETVTSGTNV	TFASGKGTTA	TVSKDDQGNI	TVKYDVNVGD	ALNVNQLQNS
BZ10	FETVTSGTKV	TFASGNGTTA	TVSKDDQGNI	TVKYDVNVGD	ALNVNQLQNS
H15	FETVTSGTKV	TFASGNGTTA	TVSKDDQGNI	TVKYDVNVGD	ALNVNQLQNS
EG329	FETVTSGTNV	TFASGKGTTA	TVSKDDQGNI	TVMYDVNVGD	ALNVNQLQNS
PMC21	FETVTSGTNV	TFASGKGTTA	TVSKDDQGNI	TVMYDVNVGD	ALNVNQLQNS
H38	FETVTSGTNV	TFASGKGTTA	TVSKDDQGNI	TVKYDVNVGD	ALNVNQLQNS
P20	FETVTSGTKV	TFASGNGTTA	TVSKDDQGNI	TVKYDVNVGD	ALNVNQLQNS
Z2491	FETVTSGTNV	TFASGKGTTA	TVSKDDQGNI	TVMYDVNVGD	ALNVNQLQNS
H41	FETVTSGTKV	TFASGNGTTA	TVSKDDQGNI	TVKYDVNVGD	ALNVNQLQNS
Consensus	FETVTSGT-V	TFASG-GTTA	TVSKDDQGNI	TV-YDVNVGD	ALNVNQLQNS

C5

FIG. 1 cont.

401

450

EG327 GWNLDKAVA GSSGKVISGN VSPSKGMDE TVNINAGNNI EITRNGKNID
 BZ198 GWNLDKAVA GSSGKVISGN VSPSKGMDE TVNINAGNNI EITRNGKNID
 BZ10 GWNLDKAVA GSSGKVISGN VSPSKGMDE TVNINAGNNI EITRNGKNID
 H15 GWNLDKAVA GSSGKVISGN VSPSKGMDE TVNINAGNNI EITRNGKNID
 EG329 GWNLDKAVA GSSGKVISGN VSPSKGMDE TVNINAGNNI EITRNGKNID
 PMC21 GWNLDKAVA GSSGKVISGN VSPSKGMDE TVNINAGNNI EITRNGKNID
 H38 GWNLDKAVA GSSGKVISGN VSPSKGMDE TVNINAGNNI EITRNGKNID
 P20 GWNLDKAVA GSSGKVISGN VSPSKGMDE TVNINAGNNI EITRNGKNID
 Z2491 GWNLDKAVA GSSGKVISGN VSPSKGMDE TVNINAGNNI EISRNGKNID
 H41 GWNLDKAVA GSSGKVISGN VSPSKGMDE TVNINAGNNI EITRNGKNID
 Consensus GWNLDKAVA GSSGKVISGN VSPSKGMDE TVNINAGNNI EI-RNGKNID

C5

451

500

EG327 IATSMTPQFS SVSLGAGADA PTLSVDEGA LNVGSKDANK PVRITNVAPG
 BZ198 IATSMAPQFS SVSLGAGADA PTLSVDEGA LNVGSKDTNK PVRITNVAPG
 BZ10 IATSMTPQFS SVSLGAGADA PTLSVDEGA LNVGSKDANK PVRITNVAPG
 H15 IATSMTPQFS SVSLGAGADA PTLSVDEGA LNVGSKDANK PVRITNVAPG
 EG329 IATSMTPQFS SVSLGAGADA PTLSVDG.DA LNVGSKDDNK PVRITNVAPG
 PMC21 IATSMTPQFS SVSLGAGADA PTLSVDG.DA LNVGSKDDNK PVRITNVAPG
 H38 IATSMTPQFS SVSLGAGADA PTLSVDDKG A LNVGSKDANK PVRITNVAPG
 P20 IATSMTPQFS SVSLGAGADA PTLSVDEGA LNVGSKDANK PVRITNVAPG
 Z2491 IATSMAPQFS SVSLGAGADA PTLSVDEGA LNVGSKDANK PVRITNVAPG
 H41 IATSMTPQFS SVSLGAGADA PTLSVDEGA LNVGSKDANK PVRITNVAPG
 Consensus IATSM-POFS SVSLGAGADA PTLSVDEGA LNVGSKDANK PVRITNVAPG
IATSM-POFS SVSLGAGADA PTLSVDEGA LNVGSKDANK PVRITNVAPG

C5

501

550

EG327 VKEGDVTNVA QLKGVQAQN LN NHIDNVDGNA RAGIAQAIAT AGLVQAYLPG
 BZ198 VKEGDVTNVA QLKGVQAQN LN NRIDNVDGNA RAGIAQAIAT AGLVQAYLPG
 BZ10 VKEGDVTNVA QLKGVQAQN LN NRIDNVDGNA RAGIAQAIAT AGLAQAYLPG
 H15 VKEGDVTNVA QLKGVQAQN LN NRIDNVDGNA RAGIAQAIAT AGLAQAYLPG
 EG329 VKEGDVTNVA QLKGVQAQN LN NRIDNVDGNA RAGIAQAIAT AGLVQAYLPG
 PMC21 VKEGDVTNVA QLKGVQAQN LN NRIDNVDGNA RAGIAQAIAT AGLVQAYLPG
 H38 VKEGDVTNVA QLKGVQAQN LN NRIDNVDGNA RAGIAQAIAT AGLVQAYLPG
 P20 VKEGDVTNVA QLKGVQAQN LN NRIDNVNGNA RAGIAQAIAT AGLAQAYLPG
 Z2491 VKEGDVTNVA QLKGVQAQN LN NRIDNVDGNA RAGIAQAIAT AGLVQAYLPG
 H41 VKEGDVTNVA QLKGVQAQN LN NRIDNVNGNA RAGIAQAIAT AGLVQAYLPG
 Consensus VKEGDVTNVA QLKGVQAQN N-IDNV-GNA RAGIAQAIAT AGL-QAYLPG

C5

551

600

EG327 KSMMAIGGGT YRGEAGYAIG YSSISDGGNW IIKGTASGNS RGHFGASASV
 BZ198 KSMMAIGGGT YRGEAGYAIG YSSISDGGNW IIKGTASGNS RGHFGASASV
 BZ10 KSMMAIGGGT YRGEAGYAIG YSSISDGGNW VIKGTASGNS RGHFGTSASV
 H15 KSMMAIGGGT YRGEAGYAIG YSSISDGGNW VIKGTASGNS RGHFGASASV
 EG329 KSMMAIGGGT YRGEAGYAIG YSSISDGGNW IIKGTASGNS RGHFGASASV
 PMC21 KSMMAIGGGT YRGEAGYAIG YSSISDGGNW IIKGTASGNS RGHFGASASV
 H38 KSMMAIGGGT YRGEAGYAIG YSSISDGGNW IIKGTASGNS RGHFGASASV
 P20 KSMMAIGGGT YLGEAGYAIG YSSISDGGNW VIKGTASGNS RGHFGTSASV
 Z2491 KSMMAIGGGT YRGEAGYAIG YSSISDGGNW IIKGTASGNS RGHFGASASV
 H41 KSMMAIGGGT YLGEAGYAIG YSSISAGGNW IIKGTASGNS RGHFGASASV
 Consensus KSMMAIGG-T Y-GEAGYAIG YSSIS--GNW -IKGTASGNS RGHFG-SASV

C5

FIG. 1 cont.

601
EG327 GYQW.
BZ198 GYQW.
BZ10 GYQW.
H15 GYQW.
EG329 GYQW.
PMC21 GYQW.
H38 GYQW.
P20 GYQW.
Z2491 GYQW.
H41 GYQW.
Consensus GYQW.
C5

FIG. 1 cont.

1 70

H15 ATGAAACAAAA TATAACCGCAT CATTGGAAAT AGTGCCTCA ATGCCCTGGGT CGTCGTATCC GAGCTCACAC
 B210 ATGAAACAAAA TATCCCGCAT CATTGGAAAT AGTGCCTCA ATGCCCTGGGT CGTCGTATCC GAGCTCACAC
 BZ198 ATGAAACAAAA TATAACCGCAT CATTGGAAAT AGTGCCTCA ATGCCCTGGGT CGTCGTATCC GAGCTCACAC
 P20 ATGAAACAAAA TATAACCGCAT CATTGGAAAT AGTGCCTCA ATGCCCTGGGT AGTCGTATCC GAGCTCACAC
 H38 ATGAAACAAAA TATAACCGCAT CATTGGAAAT AGTGCCTCA ATGCCCTGGGT CGCCGTATCC GAGCTCACAC
 Z2491 ATGAAACAAAA TATAACCGCAT CATTGGAAAT AGTGCCTCA ATGCCCTGGGT CGCCGTATCC GAGCTCACAC
 H41 ATGAAACAAAA TATAACCGCAT CATTGGAAAT AGTGCCTCA ATGCCCTGGGT CGCCGTATCC GAGCTCACAC
 EG329 ATGAAACGAAA TATGCCCAT CATTGGAAAT AGGCCCTCA ATGCCCTGGGT CGTTGTATCC GAGCTCACAC
 PMC21 ATGAAACAAAA TATAACCGCAT CATTGGAAAT AGTGCCTCA ATGCCATGGGT CGTCGTATCC GAGCTCACAC
 EG327 ATGAAACAAAA TATAACCGCAT CATTGGAAAT AGTGCCTCA ATGCCCTGGGT CGCCGTATCC GAGCTCACAC
 Consensus ATGAAAC-AAA TAT--CGCAT CATTGGAAAT AG-GCCCTCA ATGC-TGGGT -G--GTATCC GAGCTCACAC

C1

71 140

H15 GCAACCACAC CAAACGCGCC TCCGCAACCG TGGCGACCGC CGTATTGGCG ACACTGTTGT TTGCAACGGT
 B210 GCAACCACAC CAAACGCGCC TCCGCAACCG TGGCGACCGC CGTATTGGCG ACACTGTTGT TTGCAACGGT
 BZ198 GCAACCACAC CAAACGCGCC TCCGCAACCG TGGCGACCGC CGTATTGGCG ACACTGTTGT TTGCAACGGT
 P20 GCAACCACAC CAAACGCGCC TCCGCAACCG TGGCGACCGC CGTATTGGCG ACACTGCTGT CGCAACGGT
 H38 GCAACCACAC CAAACGCGCC TCCGCAACCG TGAAGACCGC CGTATTGGCG ACCTGTTGT TTGCAACGGT
 Z2491 GCAACCACAC CAAACGCGCC TCCGCAACCG TGAAGACCGC CGTATTGGCG ACACTGTTGT TTGCAACGGT
 H41 GCAACCACAC CAAACGCGCC TCCGCAACCG TGAAGACCGC CGTATTGGCG ACACTGTTGT TTGCAACGGT
 EG329 GCAACCACAC CAAACGCGCC TCCGCAACCG TGAAGACCGC CGTATTGGCG ACTCTGTTGT TTGCAACGGT
 PMC21 GCAACCACAC CAAACGCGCC TCCGCAACCG TGAAGACCGC CGTATTGGCG ACTCTGTTGT TTGCAACGGT
 EG327 GCAACCACAC CAAACGCGCC TCCGCAACCG TGGCGACCGC CGTATTGGCG ACACTGTTGT TTGCAACGGT
 Consensus GCAACCACAC CAAACGCGCC TCCGCAACCG TG-GACCGC CGTATTGGCG AC-CTG-TGT --GCAACGGT

C1

141 210

H15 TCAGGGCAAT GCTACCGATG ACGAC..... GATTTA TATTTAGAAC CCGTACAACG CACTGCTGTC
 B210 TCAGGGCAAT GCTACCGATG ACGAC..... GATTTA TATTTAGAAC CCGTACAACG CACTGCTGTC
 BZ198 TCAGGGCAAT GCTACCGATG ACGAC..... GATTTA TATTTAGAAC CCGTACAACG CACTGCTGTC
 P20 TCAGGGCAAT GCTACCGATA CCGAT..... GAAGATGAA GAGTTAGAAC CCGTAGCACG CTCTGCTCTG
 H38 TCAGGGCAAT GCTACCGATG AAGAT..... GAAGAAGAA GAGTTAGAAC CCGTAGCACG CTCTGCTCTG
 Z2491 TCAGGGCAAT GCTACCGATG AAGAT..... GAAGAAGAA GAGTTAGAAC CCGTACAACG CTCTGCTGTA
 H41 TCAGGGCAAT GCTACCGATG AAGAT..... GAAGAAGAA GAGTTAGAAC CCGTACAACG CTCTG...TC
 EG329 TCAGGGCAAGT GCTAACAAATG AAGAGCAAGA AGAAGATTTA TATTTAGACC CCGTGTACAG CACTGTTGCC
 PMC21 TCAGGGCAAGT GCTAACAAATG AAGAGCAAGA AGAAGATTTA TATTTAGACC CCGTACAACG CACTGTTGCC
 EG327 TCAGGGGAGT ACTACCGATG ACGAC..... GATTTA TATTTAGAAC CCGTACAACG CACTGCTGTC
 Consensus TCAGG-C-A-T -CTA-C-AT- --GA-----GA---A-A-TTAA- CCGT---ACG C-CTG-----

C1

V1

211 280

H15 GTGTTGAGCT TCCGTTCCGA TAAAGAAGGC ACGGGAGAAA AAGAAGGTAC AGAAGA...T TCAAATTGGG
 B210 GTGTTGAGCT TCCGTTCCGA TAAAGAAGGC ACGGGAGAAA AAGAAGGTAC AGAAGA...T TCAAATTGGG
 BZ198 GTGTTGAGCT TCCGTTCCGA TAAAGAAGGC ACGGGAGAAA AAGAAGGTAC AGAAGA...T TCAAATTGGG
 P20 GTGTTGCAAT TCATGATCGA TAAAGAAGGC AATGGAGAAA TCGAATCTAC AGGAGA...T ATAGGTTGG
 H38 GTGTTGCAAT TCATGATCGA TAAAGAAGGC AATGGAGAAA AGGAATCTAC AGGAAA...T ATAGGTTGG
 Z2491 GGG..AGCAT TCAAG.CCAG TATGGAAGGC AGCGGCAAT TGGAAACGAT ATCAT....T ATCAATGACT
 H41 GTAGGGAGCA TTCAAGCCAG TATGGAAGGC AGCGTCAAT TGGAAACGAT A..... TCATTATCAA
 EG329 GTGTTGATAG TCAATTCCGA TAAAGAAGGC ACGGGAGAAA AGAAGAAAAGT AGAAGAAAAT TCAGATTGG
 PMC21 GTGTTGATAG TCAATTCCGA TAAAGAAGGC ACGGGAGAAA AGAAGAAAAGT AGAAGAAAAT TCAGATTGG
 EG327 GTGTTGAGCT TCCGTTCCGA TAAAGAAGGC ACGGGAGAAA AAGAAGTTAC AGAAGA...T TCAAATTGGG
 Consensus G-----T-----C-- TA-GAAGGC A--G-GAA- --GAA---- A-----

V1

FIG. 2

		281	
H15	CGATATATT CGACGGAGAA AGAGTACTAA AAGCCGGAGC AATCACCTCT AAGCCGGCG ACAACCTGAA		
BZ10	CGATATATT CGACGGAGAA AGAGTACTAA AAGCCGGAGC AATCACCTCT AAGCCGGCG ACAACCTGAA		
BZ198	CGATATATT CGACGGAGAA AGAGTACTAA AAGCCGGAGC AATCACCTCT AAGCCGGCG ACAACCTGAA		
P20	GTATATATT CGACGATCAC AACACTCTAC ACGGCGCAAC CGTTACCCCTC AAAGCCGGCG ACAACCTGAA		
H38	GTATATATT CGACAAATCAC AACACTCTAC ACGGCGCAAC CGTTACCCCTC AAAGCCGGCG ACAACCTGAA		
Z2491	AACGACACCA AGGAATTGT AGACCCATAC ATAGTA.... GTTACCCCTC AAAGCCGGCG ACAACCTGAA		
H41	TGACTAACGA CAGCAAGGA TTTGTAGACC CATACATAGT AGTTACCCCTC AAAGCCGGCG ACAACCTGAA		
EG329	CGATATATT CAACGGAGAA GGAGTACTAA CAGCCAGAGA AATCACCTCT AAGCCGGCG ACAACCTGAA		
PMC21	CGATATATT CAACGGAGAA GGAGTACTAA CAGCCAGAGA AATCACCTCT AAGCCGGCG ACAACCTGAA		
EG327	GAGTATATT CGACAAAGAA GGAGTACTAA CAGCCGGAGA AATCACCTCT AAGCCGGCG ACAACCTGAA		
Consensus	-----A-----	V1	C2
		420	
H15	AATCAAACAA AACACCAATG AAAACACCA TGAAAACACC AATGACAGTA GCTTCACCTA CTCCCTGAAA		
BZ10	AATCAAACAA AACACCAATG AAAACACCA TGAAAACACC AATGACAGTA GCTTCACCTA CTCCCTGAAA		
BZ198	AATCAAACAA AACACCAATG AAAACACC.. AATGACAGTA GCTTCACCTA CTCCCTGAAA		
P20	AATCAAACAA AGCGCCAAG A..... CTTACCTA CTGGCTGAAA		
H38	AATCAAACAA AACACCAATAA AAAACACCA TGAAAACACC AATGACAGTA GCTTCACCTA CTGGCTGAAA		
Z2491	AATCAAACAA AACACCAATG AAAACACC.. AATGCCAGTA GCTTCACCTA CTGGCTGAAA		
H41	AATCAAACAA AACACCAATG AAAACACC.. AATGCCAGTA GCTTCACCTA CTGGCTGAAA		
EG329	AATCAAACAA AAC..... G..... GCACAA ACTTCACCTA CTGGCTGAAA		
PMC21	AATCAAACAA AAC..... G..... GCACAA ACTTCACCTA CTGGCTGAAA		
EG327	AATCAAACAA AACACCAATG AAAACACC.. AATGCCAGTA GCTTCACCTA CTGGCTGAAA		
Consensus	ANTCAAACAA A-C-----	C2	V2
		490	
H15	AAAGACCTCA CAGATCTGAC CAGTGTGAA ACTGAAAAAA TATCGTTGG CGCRAACGGT AATAAAGTCA		
BZ10	AAAGACCTCA CAGATCTGAC CAGTGTGAA ACTGAAAAAA TATCGTTGG CGCRAACGGT AATAAAGTCA		
BZ198	AAAGACCTCA CAGATCTGAC CAGTGTGAA ACTGAAAAAA TATCGTTGG CGCRAACGGT AATAAAGTCA		
P20	AAAGAGCTGA AAGACCTGAC CAGTGTGAA ACTGAAAAAA TATCGTTGG CGCRAACGGT AATAAAGTCA		
H38	AAAGACCTCA CAGATCTGAC CAGTGTGAA ACTGAAAAAA TATCGTTGG CGCRAACGGC AATAAAGTCA		
Z2491	AAAGACCTCA CAGGCCTGAT CAATGTTGAA ACTGAAAAAA TATCGTTGC CGCRAACGGC AAGAAAGTCA		
H41	AAAGACCTCA CAGGCCTGAT CAATGTTGAA ACTGAAAAAA TATCGTTGC CGCRAACGGC AAGAAAGTCA		
EG329	AAAGACCTCA CAGATCTGAC CAGTGTGAA ACTGAAAAAA TATCGTTAG CGCRAACGGC AATAAAGTCA		
PMC21	AAAGACCTCA CAGATCTGAC CAGTGTGAA ACTGAAAAAA TATCGTTAG CGCRAACGGC AATAAAGTCA		
EG327	AAAGACCTCA CAGATCTGAC CAGTGTGAA ACTGAAAAAA TATCGTTAG CGCRAACGGC AATAAAGTCA		
Consensus	AAAGA-CT-A -AG--CTGA- CA-TGTG-A ACTGAAAAAA TATCGTT-G CGCRAAC-G- AA-AAAGTCA	C3	C3
		560	
H15	ACATCACAAAG CGACACCAAA GGCTTGAAATT TTGCGAAAGA AACGGCTGGG ACCAACGGCG ACCCCACGGT		
BZ10	ACATCACAAAG CGACACCAAA GGCTTGAAATT TTGCGAAAGA AACGGCTGGG ACCAACGGCG ACCCCACGGT		
BZ198	ACATCACAAAG CGACACCAAA GGCTTGAAATT TTGCGAAAGA AACGGCTGGG ACCAACGGCG ACCCCACGGT		
P20	ACATCACAAAG CGACACCAAA GGCTTGAAATT TTGCGAAAGA AACGGCTGGG ACCAACGGCG ACCCCACGGT		
H38	ACATCACAAAG CGACACCAAA GGCTTGAAATT TCGGAAAGA AACGGCTGGG ACCAACGGCG ACACCACGGT		
Z2491	ACATCATAAAG CGACACCAAA GGCTTGAAATT TCGGAAAGA AACGGCTGGG ACCAACGGCG ACACCACGGT		
H41	ACATCATAAAG CGACACCAAA GGCTTGAAATT TCGGAAAGA AACGGCTGGG ACCAACGGCG ACACCACGGT		
EG329	ACATCACAAAG CGACACCAAA GGCTTGAAATT TTGCGAAAGA AACGGCTGGG ACCAACGGCG ACACCACGGT		
PMC21	ACATCACAAAG CGACACCAAA GGCTTGAAATT TTGCGAAAGA AACGGCTGGG ACCAACGGCG ACACCACGGT		
EG327	ACATCACAAAG CGACACCAAA GGCTTGAAATT TCGGAAAGA AACGGCTGAG ACCAACGGCG ACACCACGGT		
Consensus	ACATCA-AAG CGACACCAAA GGCTTGAAATT T-GCGAA-A AACGGCTG-G AC-AACGGCG AC-CCACGGT	C3	C3
		630	
H15	TCATCTGAAC GGTATCGGTT CGACTTTGAC CGATACGCTG CTGAATACCG GAGGGACCCAC AAACGTAACC		
BZ10	TCATCTGAAC GGTATCGGTT CGACTTTGAC CGATACGCTG CTGAATACCG GAGGGACCCAC AAACGTAACC		
BZ198	TCATCTGAAC GGTATCGGTT CGACTTTGAC CGATACGCTG CTGAATACCG GAGGGACCCAC AAACGTAACC		
P20	TCATCTGAAC GGTATCGGTT CGACTTTGAC CGATACGCTT CGGGGTCTT CTGCTTCTCA CGTTGATGCG		
H38	TCATCTGAAC GGTATCGGTT CGACTTTGAC CGATACGCTT CTGAATACCG GAGGGACCCAC AAACGTAACC		
Z2491	TCATCTGAAC GGTATCGGTT CGACTTTGAC CGATACGCTT CGGGGTCTT CTGCTTCTCA CGTTGATGCG		
H41	TCATCTGAAC GGTATCGGTT CGACTTTGAC CGATATGCTG CTGAATACCG GAGGGACCCAC AAACGTAACC		
EG329	TCATCTGAAC GGTATCGGTT CGACTTTGAC CGATACGCTG CTGAATACCG GAGGGACCCAC AAACGTAACC		
PMC21	TCATCTGAAC GGTATCGGTT CGACTTTGAC CGATACGCTG CTGAATACCG GAGGGACCCAC AAACGTAACC		
EG327	TCATCTGAAC GGTATCGGTT CGACTTTGAC CGATACGCTG CTGAATACCG GAGGGACCCAC AAACGTAACC		
Consensus	TCATCTGAAC GGTATCGGTT CGACTTTGAC CGATA-GCT- --G-T-C-- --G-C--- --G---C-	C3	V3

FIG. 2 cont.

<p>631</p> <p>H15 AACGACAACG TTACCGATGA CGAGAAAAAA CGTGGGGCAA CGCTTAAGA CGTATTAAAC GCAGGCTGGA BZ10 AACGACAACG TTACCGATGA CGAGAAAAAA CGTGGGGCAA CGCTTAAGA CGTATTAAAC GCAGGCTGGA BZ198 AACGACAACG TTACCGATGA CGAGAAAAAA CGTGGGGCAA CGCTTAAGA CGTATTAAAC GCAGGCTGGA P20 GGTAAACAAA GTACACATTA C.....ACT CGTGCAAGCA GTATTAAGGA TGTGTGAAAT CGGGCTGGA H38 AACGACAACG TTACCGATGA CGAGAAAAAA CGTGGGGCAA CGCTTAAGA CGTATTAAAC GCAGGCTGGA 22491 GGTAAACAAA GTACACATTA C.....ACT CGTGCAAGCA GTATTAAGGA TGTGTGAAAT CGGGCTGGA H41 AACGACAACG TTACCGATGA CGAGAAAAAA CGTGGGGCAA CGCTTAAGA CGTATTAAAC GCAGGCTGGA EG329 AACGACAACG TTACCGATGA CGAGAAAAAA CGTGGGGCAA CGCTTAAGA CGTATTAAAC GCAGGCTGGA PMC21 AACGACAACG TTACCGATGA CGAGAAAAAA CGTGGGGCAA CGCTTAAGA CGTATTAAAC GCAGGCTGGA EG327 AACGACAACG TTACCGATGA CGAGAAAAAA CGTGGGGCAA CGCTTAAGA CGTATTAAAC GCAGGCTGGA Consensus <u>---AC-A-- -TAC--AT-A C-----A-</u> CGTC-GCAA G-TTAA-GA -GT-TT-AA- GC-GG-TGGA</p>	<p>700</p> <p>V3 C4</p>
<p>701</p> <p>H15 ACATTAAGG CGTAAACCC GTACAACAG CT.....TC CGATAACGT GATTCGTCC GCACCTACGA BZ10 ACATTAAGG CGTAAACCC GTACAACAG CT.....TC CGATAACGT GATTCGTCC GCACCTACGA BZ198 ACATTAAGG CGTAAACCC GTACAACAG CT.....TC CGATAACGT GATTCGTCC GCACCTACGA P20 ATATTAAGGG TGTAAAACG GTGTCAACAG CTGGTCAATC AGAAAATGTC GATTCGTCC GCACCTACGA H38 ACATTAAGG CGTAAACCC GTACAACAG CT.....TC CGATAACGT GATTCGTCC ACACTTACGA 22491 ATATTAAGGG TGTAAAACG GTGTCAACAG CTGGTCAATC AGAAAATGTC GATTCGTCC GCACCTACGA H41 ACATTAAGG CGTAAACCC GTACAACAG CT.....TC CGATAACGT GATTCGTCC GCACCTACGA EG329 ACATTAAGG CGTAAACCC GTACAACAG CT.....TC CGATAACGT GATTCGTCC GCACCTACGA PMC21 ACATTAAGG CGTAAACCC GTACAACAG CT.....TC CGATAACGT GATTCGTCC GCACCTACGA EG327 ACATTAAGG CGTAAACCC GTACAACAG CT.....TC CGATAACGT GATTCGTCC GCACCTACGA Consensus <u>A-TTAA-GG -GTAAA-C- GG-CAACA- CT-----TC -GA-AA-GT GATTCGTCC -GACTTACGA</u></p>	<p>770</p> <p>C4 V4 C5</p>
<p>771</p> <p>H15 CACAGTCGAG TTCTTGAGCC CAGATACGAA AACAAACGACT GTTAATGTGG AAAGCAAAAG CAACGGCAAG BZ10 CACAGTCGAG TTCTTGAGCC CAGATACGAA AACAAACGACT GTTAATGTGG AAAGCAAAAG CAACGGCAAG BZ198 CACAGTCGAG TTCTTGAGCC CAGATACGAA AACAAACGACT GTTAATGTGG AAAGCAAAAG CAACGGCAAG P20 CACAGTCGAG TTCTTGAGCC CAGATACGAA AACAAACGACT GTTAATGTGG AAAGCAAAAG CAACGGCAAG H38 CACAGTCGAG TTCTTGAGCC CAGATACGAA AACAAACGACT GTTAATGTGG AAAGCAAAAG CAACGGCAAG 22491 CACAGTCGAG TTCTTGAGCC CAGATACGAA AACAAACGACT GTTAATGTGG AAAGCAAAAG CAACGGCAAG H41 CACAGTCGAG TTCTTGAGCC CAGATACGAA AACAAACGACT GTTAATGTGG AAAGCAAAAG CAACGGCAAG EG329 CACAGTCGAG TTCTTGAGCC CAGATACGAA AACAAACGACT GTTAATGTGG AAAGCAAAAG CAACGGCAAG PMC21 CACAGTCGAG TTCTTGAGCC CAGATACGAA AACAAACGACT GTTAATGTGG AAAGCAAAAG CAACGGCAAG EG327 CACAGTCGAG TTCTTGAGCC CAGATACGAA AACAAACGACT GTTAATGTGG AAAGCAAAAG CAACGGCAAG Consensus <u>CACAGTCGAG TTCTTGAGCC CAGATACGAA AACAAACGACT GTTAATGTGG AAAGCAAAAG CAACGGCAAG</u></p>	<p>840</p> <p>C5</p>
<p>841</p> <p>H15 AAAACCGAAG TTAAAATCGG TGCGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA BZ10 AAAACCGAAG TTAAAATCGG TGCGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA BZ198 AAAACCGAAG TTAAAATCGG TGCGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA P20 AGAACCGAAG TTAAAATCGG TGCGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA H38 AGAACCGAAG TTAAAATCGG TGCGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA 22491 AGAACCGAAG TTAAAATCGG TGCGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA H41 AAAACCGAAG TTAAAATCGG TGCGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA EG329 AAAACCGAAG TTAAAATCGG TGCGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA PMC21 AAAACCGAAG TTAAAATCGG TGCGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA EG327 AGAACCGAAG TTAAAATCGG TGCGAAGACT TCTGTTATCA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA Consensus <u>A-AAACCGAAG TTAAAATCGG TGCGAAGACT TCTGTTATCA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA</u></p>	<p>910</p> <p>C5</p>
<p>911</p> <p>H15 AAGGCCAAGA CGAGAATGGT TCTTCTACAG ACGAAGGGCA AGGCTTAGTG ACTGCRAAAG AAGTGATTGA BZ10 AAGGCCAAGA CGAGAATGGT TCTTCTACAG ACGAAGGGCA AGGCTTAGTG ACTGCRAAAG AAGTGATTGA BZ198 AAGGCCAAGA CGAGAATGGT TCTTCTACAG ACGAAGGGCA AGGCTTAGTG ACTGCRAAAG AAGTGATTGA P20 AAGGCCAAGA CGAGAATGGT TCTTCTACAG ACGAAGGGCA AGGCTTAGTG ACTGCRAAAG AAGTGATTGA H38 AAGGCCAAGA CGAGAATGGT TCTTCTACAG ACGAAGGGCA AGGCTTAGTG ACTGCRAAAG AAGTGATTGA 22491 AAGGCCAAGA CGAGAATGGT TCTTCTACAG ACGAAGGGCA AGGCTTAGTG ACTGCRAAAG AAGTGATTGA H41 AAGGCCAAGA CGAGAATGGT TCTTCTACAG ACGAAGGGCA AGGCTTAGTG ACTGCRAAAG AAGTGATTGA EG329 AAGGCCAAGA CGAGAATGGT TCTTCTACAG ACGAAGGGCA AGGCTTAGTG ACTGCRAAAG AAGTGATTGA PMC21 AAGGCCAAGA CGAGAATGGT TCTTCTACAG ACGAAGGGCA AGGCTTAGTG ACTGCRAAAG AAGTGATTGA EG327 AAGGCCAAGA CGAGAATGGT TCTTCTACAG ACGAAGGGCA AGGCTTAGTG ACTGCRAAAG AAGTGATTGA Consensus <u>AAG-CAAAG- CGAGAATG-T TCTTCTACAG AC-AAGGGCA AGGCTTAGTG ACTGCRAAAG AAGTGATTGA</u></p>	<p>980</p> <p>C5</p>

FIG. 2 cont.

	981		1050				
H15	TGCAGTAAAC	AAGGCTGGTT	GGAGAATGAA	ACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
BZ10	TGCAGTAAAC	AAGGCTGGTT	GGAGAATGAA	ACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
BZ198	TGCAGTAAAC	AAGGCTGGTT	GGAGAATGAA	ACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
P20	TGCAGTAAAC	AAGGCTGGTT	GGAGAATGAA	ACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
H38	TGCAGTAAAC	AAGGCTGGTT	GGAGAATGAA	ACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
Z2491	TGCAGTAAAC	AAGGCTGGTT	GGAGAATGAA	ACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
H41	TGCAGTAAAC	AAGGCTGGTT	GGAGAATGAA	ACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
EG329	TGCAGTAAAC	AAGGCTGGTT	GGAGAATGAA	ACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
PMC21	TGCAGTAAAC	AAGGCTGGTT	GGAGAATGAA	ACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
EG327	TGCAGTAAAC	AAGGCTGGTT	GGAGAATGAA	ACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
Consensus	<u>TGCAGTAAAC</u>	<u>AAGGCTGGTT</u>	<u>GGAGAATGAA</u>	<u>ACAACAACC</u>	<u>GCTAATGGTC</u>	<u>AAACAGGTCA</u>	<u>AGCTGACAAG</u>
		C5					
	1051		1120				
H15	TTTGAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAACACTCGG	ACTGTAAGTA
BZ10	TTTGAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAACACTCGG	ACTGTAAGTA
BZ198	TTTGAACCG	TTACATCAGG	CACAAATGTA	ACCTTTGCTA	GTGGTAAGGG	TACAACACTCGG	ACTGTAAGTA
P20	TTTGAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAACACTCGG	ACTGTAAGTA
H38	TTTGAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAAGGG	TACAACACTCGG	ACTGTAAGTA
Z2491	TTTGAACCG	TTACATCAGG	CACAAATGTA	ACCTTTGCTA	GTGGTAAGGG	TACAACACTCGG	ACTGTAAGTA
H41	TTTGAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAAGGG	TACAACACTCGG	ACTGTAAGTA
EG329	TTTGAACCG	TTACATCAGG	CACAAATGTA	ACCTTTGCTA	GTGGTAAGGG	TACAACACTCGG	ACTGTAAGTA
PMC21	TTTGAACCG	TTACATCAGG	CACAAATGTA	ACCTTTGCTA	GTGGTAAGGG	TACAACACTCGG	ACTGTAAGTA
EG327	TTTGAACCG	TTACATCAGG	CACAAA-GTA	ACCTTTGCTA	GTGGTAAGGG	TACAACACTCGG	ACTGTAAGTA
Consensus	<u>TTTGAACCG</u>	<u>TTACATCAGG</u>	<u>CACAAA-GTA</u>	<u>ACCTTTGCTA</u>	<u>GTGGTAAGGG</u>	<u>TACAACACTCGG</u>	<u>ACTGTAAGTA</u>
		C5					
	1121		1190				
H15	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCCCCGAT	GCCCTAAACG	TCAATCAGCT
BZ10	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCCCCGAT	GCCCTAAACG	TCAATCAGCT
BZ198	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCCCCGAT	GCCCTAAACG	TCAATCAGCT
P20	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCCCCGAT	GCCCTAAACG	TCAATCAGCT
H38	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCCCCGAT	GCCCTAAACG	TCAATCAGCT
Z2491	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCCCCGAT	GCCCTAAACG	TCAATCAGCT
H41	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCCCCGAT	GCCCTAAACG	TCAATCAGCT
EG329	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCCCCGAT	GCCCTAAACG	TCAATCAGCT
PMC21	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCCCCGAT	GCCCTAAACG	TCAATCAGCT
EG327	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCCCCGAT	GCCCTAAACG	TCAATCAGCT
Consensus	<u>AAGATGATCA</u>	<u>AGGCAACATC</u>	<u>ACTGTTAAGT</u>	<u>ATGATGTAAA</u>	<u>TGTCCCCGAT</u>	<u>GCCCTAAACG</u>	<u>TCAATCAGCT</u>
		C5					
	1191		1260				
H15	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	ACCGGTTGCA	GGTTCTTCGG	GC _{AA} AGTCAT	CAGCGGCAAT
BZ10	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	ACCGGTTGCA	GGTTCTTCGG	GC _{AA} AGTCAT	CAGCGGCAAT
BZ198	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	ACCGGTTGCA	GGTTCTTCGG	GC _{AA} AGTCAT	CAGCGGCAAT
P20	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	ACCGGTTGCA	GGTTCTTCGG	GC _{AA} AGTCAT	CAGCGGCAAT
H38	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	ACCGGTTGCA	GGTTCTTCGG	GC _{AA} AGTCAT	CAGCGGCAAT
Z2491	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	ACCGGTTGCA	GGTTCTTCGG	GC _{AA} AGTCAT	CAGCGGCAAT
H41	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	ACCGGTTGCA	GGTTCTTCGG	GC _{AA} AGTCAT	CAGCGGCAAT
EG329	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	ACCGGTTGCA	GGTTCTTCGG	GC _{AA} AGTCAT	CAGCGGCAAT
PMC21	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	ACCGGTTGCA	GGTTCTTCGG	GC _{AA} AGTCAT	CAGCGGCAAT
EG327	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	ACCGGTTGCA	GGTTCTTCGG	GC _{AA} AGTCAT	CAGCGGCAAT
Consensus	<u>GCAAAACAGC</u>	<u>GGTTGGAATT</u>	<u>TGGATTCCAA</u>	<u>ACCGGTTGCA</u>	<u>GGTTCTTCGG</u>	<u>GC_{AA}AGTCAT</u>	<u>CAGCGGCAAT</u>
		C5					
	1261		1330				
H15	GTTTCGGCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
BZ10	GTTTCGGCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
BZ198	GTTTCGGCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
P20	GTTTCGGCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
H38	GTTTCGGCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
Z2491	GTTTCGGCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
H41	GTTTCGGCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
EG329	GTTTCGGCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
PMC21	GTTTCGGCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
EG327	GTTTCGGCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
Consensus	<u>GTTTCGGCGA</u>	<u>GCAAGGGAAA</u>	<u>GATGGATGAA</u>	<u>ACCGTCAACA</u>	<u>TTAATGCCGG</u>	<u>CAACAACATC</u>	<u>GAGATTACCC</u>
		C5					

FIG. 2 cont.

	1331		1400				
H15	GCAACGGCAA	AAATATCGAC	ATGCCACTT	CGATGACCCC	GCAATTTC	AGCGTTTGC	TCCGGCGCGG
BZ10	GCAACGGCAA	AAATATCGAC	ATGCCACTT	CGATGACCCC	GCAATTTC	AGCGTTTGC	TCCGGCGCGG
BZ198	GCAACGGTAA	AAATATCGAC	ATGCCACTT	CGATGGGCC	GCAATTTC	AGCGTTTGC	TCCGGCGCGG
P20	GCAACGGCAA	AAATATCGAC	ATGCCACTT	CGATGACCCC	GCAATTTC	AGCGTTTGC	TCCGGCGCGG
H38	GCAACGGTAA	AAATATCGAC	ATGCCACTT	CGATGACCCC	GCAATTTC	AGCGTTTGC	TCCGGCGCGG
Z2491	GCAACGGTAA	AAATATCGAC	ATGCCACTT	CGATGGGCC	GCAATTTC	AGCGTTTGC	TCCGGCGCGG
H41	GCAACGGCAA	AAATATCGAC	ATGCCACTT	CGATGACCCC	GCAATTTC	AGCGTTTGC	TCCGGCGCGG
EG329	GCAACGGTAA	AAATATCGAC	ATGCCACTT	CGATGACCCC	GCAATTTC	AGCGTTTGC	TCCGGCGCGG
PMC21	GCAACGGTAA	AAATATCGAC	ATGCCACTT	CGATGACCCC	GCAATTTC	AGCGTTTGC	TCCGGCGCGG
EG327	GCAACGGCAA	AAATATCGAC	ATGCCACTT	CGATGACCCC	GCAATTTC	AGCGTTTGC	TCCGGCGCGG
Consensus	<u>GCAACGG-<u>AA</u></u>	<u>AAATATCGAC</u>	<u>ATGCCACTT</u>	<u>CGATG-C-CC</u>	<u>GCA-TTTTC</u>	<u>AGCGTTTGC</u>	<u>TCCG-GCGGG</u>
		C5					
	1401		1470				
H15	GGCGGATGCG	CCCACTTAA	GGGTGGATGA	CGAGGGCGCG	TTGAATGTC	GCAGCAAGGA	TGCCAACAAA
BZ10	GGCGGATGCG	CCCACTTAA	GGGTGGATGA	CGAGGGCGCG	TTGAATGTC	GCAGCAAGGA	TGCCAACAAA
BZ198	GGCGGATGCG	CCCACTTAA	GGGTGGATGA	CGAGGGCGCG	TTGAATGTC	GCAGCAAGGA	TACCAACAAA
P20	GGCGGATGCG	CCCACTTAA	GGGTGGATGA	CGAGGGCGCG	TTGAATGTC	GCAGCAAGGA	TGCCAACAAA
H38	GGCGGATGCG	CCCACTTAA	GGGTGGATGA	CAAGGGCGCG	TTGAATGTC	GCAGCAAGGA	TGCCAACAAA
Z2491	GGCAGATGCG	CCCACTTAA	GGGTGGATGA	CGAGGGCGCG	TTGAATGTC	GCAGCAAGGA	TGCCAACAAA
H41	GGCGGATGCG	CCCACTTAA	GGGTGGATGA	CGAGGGCGCG	TTGAATGTC	GCAGCAAGGA	TGCCAACAAA
EG329	GGCGGATGCG	CCCACTTAA	GGGTGGATGA	CGAGGGCGCG	TTGAATGTC	GCAGCAAGGA	TGCCAACAAA
PMC21	GGCGGATGCG	CCCACTTAA	GGGTGGATGA	CGAGGGCGCG	TTGAATGTC	GCAGCAAGGA	TGCCAACAAA
EG327	GGCGGATGCG	CCCACTTAA	GGGTGGATGA	CGAGGGCGCG	TTGAATGTC	GCAGCAAGGA	TGCCAACAAA
Consensus	<u>GGC-GATGCG</u>	<u>CCCACTT-A</u>	<u>GGGTGGAT-</u>	<u>--GG-CG-</u>	<u>TTGAATGTC</u>	<u>GCAGCAAG-A</u>	<u>--CAACAAA</u>
		C5					
	1471		1540				
H15	CCCGTCCGCA	TTACCAATGT	CGCCCCGGGC	GTTAAAGAGG	GGGATTTAC	AAACGTGCGA	CACTTAAAG
BZ10	CCCGTCCGCA	TTACCAATGT	CGCCCCGGGC	GTTAAAGAGG	GGGATTTAC	AAACGTGCGA	CACTTAAAG
BZ198	CCCGTCCGCA	TTACCAATGT	CGCCCCGGGC	GTTAAAGAGG	GGGATTTAC	AAACGTGCGA	CACTTAAAG
P20	CCCGTCCGCA	TTACCAATGT	CGCCCCGGGC	GTTAAAGAGG	GGGATTTAC	AAACGTGCGA	CACTTAAAG
H38	CCCGTCCGCA	TTACCAATGT	CGCCCCGGGC	GTTAAAGAGG	GGGATTTAC	AAACGTGCGA	CACTTAAAG
Z2491	CCCGTCCGCA	TTACCAATGT	CGCCCCGGGC	GTTAAAGAGG	GGGATTTAC	AAACGTGCGA	CACTTAAAG
H41	CCCGTCCGCA	TTACCAATGT	CGCCCCGGGC	GTTAAAGAGG	GGGATTTAC	AAACGTGCGG	CACTTAAAG
EG329	CCCGTCCGCA	TTACCAATGT	CGCCCCGGGC	GTTAAAGAGG	GGGATTTAC	AAACGTGCGA	CACTTAAAG
PMC21	CCCGTCCGCA	TTACCAATGT	CGCCCCGGGC	GTTAAAGAGG	GGGATTTAC	AAACGTGCGA	CACTTAAAG
EG327	CCCGTCCGCA	TTACCAATGT	CGCCCCGGGC	GTTAAAGAGG	GGGATTTAC	AAACGTGCGA	CACTTAAAG
Consensus	<u>CCCGTCCGCA</u>	<u>TTACCAATGT</u>	<u>CGCCCCGGGC</u>	<u>GTTAAAGAGG</u>	<u>GGGATTTAC</u>	<u>AAACGTGCG-</u>	<u>CACTTAAAG</u>
		C5					
	1541		1610				
H15	GTGTGGCGCA	AAACCTGAAC	AACCGCATCG	ACAATGTGGA	CGGCAACGGC	CGCGCGGGTA	TGCCCAAGC
BZ10	GTGTGGCGCA	AAACCTGAAC	AACCGCATCG	ACAATGTGGA	CGGCAACGGC	CGCGCGGGTA	TGCCCAAGC
BZ198	GTGTGGCGCA	AAACCTGAAC	AACCGCATCG	ACAATGTGGA	CGGCAACGGC	CGTGCGGGCA	TGCCCAAGC
P20	GTGTGGCGCA	AAACCTGAAC	AACCGCATCG	ACAATGTGGA	CGGCAACGGC	CGTGCGGGTA	TGCCCAAGC
H38	GTGTGGCGCA	AAACCTGAAC	AACCGCATCG	ACAATGTGGA	CGGCAACGGC	CGTGCGGGCA	TGCCCAAGC
Z2491	GTGTGGCGCA	AAACCTGAAC	AACCGCATCG	ACAATGTGGA	CGGCAACGGC	CGTGCGGGCA	TGCCCAAGC
H41	GTGTGGCGCA	AAACCTGAAC	AACCGCATCG	ACAATGTGGA	CGGCAACGGC	CGTGCGGGCA	TGCCCAAGC
EG329	GTGTGGCGCA	AAACCTGAAC	AACCGCATCG	ACAATGTGGA	CGGCAACGGC	CGTGCGGGCA	TGCCCAAGC
PMC21	GTGTGGCGCA	AAACCTGAAC	AACCGCATCG	ACAATGTGGA	CGGCAACGGC	CGTGCGGGCA	TGCCCAAGC
EG327	GTGTGGCGCA	AAACCTGAAC	AACCATGAC	ACAATGTGGA	CGGCAACGGC	CGTGCGGGCA	TGCCCAAGC
Consensus	<u>G-GTGTGGCGCA</u>	<u>AAACCTGAAC</u>	<u>AACCG-CATCG</u>	<u>ACAATGTG-A</u>	<u>CGGCAACGGC</u>	<u>CG-GCGG-A</u>	<u>TGCCCAAGC</u>
		C5					
	1611		1680				
H15	GATTGCAACC	GCAGGTTTGG	CTCAGGCGTA	TTTGGCCCGC	AAGAGTATGA	TGGCGATCGG	CGCGCGTACT
BZ10	GATTGCAACC	GCAGGTTTGG	CTCAGGCGTA	TTTGGCCCGC	AAGAGTATGA	TGGCGATCGG	CGCGCGTACT
BZ198	GATTGCAACC	GCAGGTTCTGG	TTCAAGGCGTA	TCTGCCCCGGC	AAGAGTATGA	TGGCGATCGG	CGCGCGACACT
P20	GATTGCAACC	GCAGGTTTGG	CTCAGGCGTA	TTTGGCCCGC	AAGAGTATGA	TGGCGATCGG	CGCGCGTACT
H38	GATTGCAACC	GCAGGTTCTGG	TTCAAGGCGTA	TCTGCCCCGGC	AAGAGTATGA	TGGCGATCGG	CGCGCGGACT
Z2491	GATTGCAACC	GCAGGTTCTGG	TTCAAGGCGTA	TCTGCCCCGGC	AAGAGTATGA	TGGCGATCGG	CGCGCGGACT
H41	GATTGCAACC	GCAGGTTCTGG	TTCAAGGCGTA	TCTGCCCCGGC	AAGAGTATGA	TGGCGATCGG	CGCGCGGACT
EG329	GATTGCAACC	GCAGGTTCTGG	TTCAAGGCGTA	TCTGCCCCGGC	AAGAGTATGA	TGGCGATCGG	CGCGCGGACT
PMC21	GATTGCAACC	GCAGGTTCTGG	TTCAAGGCGTA	TCTGCCCCGGC	AAGAGTATGA	TGGCGATCGG	CGCGCGGACT
EG327	GATTGCAACC	GCAGGTTCTGG	TTCAAGGCGTA	TCTGCCCCGGC	AAGAGTATGA	TGGCGATCGG	CGCGCGGACT
Consensus	<u>GATTGCAACC</u>	<u>GCAGG-T-CTGG</u>	<u>TTCAAGGCGTA</u>	<u>TCTGCCCCGGC</u>	<u>AAGAGTATGA</u>	<u>TGGCGATCGG</u>	<u>CGCGCGGACT</u>
		C5					

FIG. 2 cont.

1681 1750
 H15 TATCGCGGCG AAGCCGGTTA CGCCATCGGC TACTCGAGCA TTTCTGACAC TGGGAATTGG GTTATCAAAG
 BZ10 TATCGCGGCG AAGCCGGTTA CGCCATCGGC TACTCGAGCA TTTCTGACAC TGGGAATTGG GTTATCAAAG
 BZ198 TATCGCGGCG AAGCCGGTTA CGCCATCGGC TACTCAAGTA TTTCCGACGG CGGAAATTGG ATTATCAAAG
 P20 TATCTCGCGGCG AAGCCGGTTA CGCCATCGGC TACTCGAGCA TTTCTGACAC TGGGAATTGG GTTATCAAAG
 H38 TATCGCGGCG AAGCCGGTTA CGCCATCGGC TACTCAGTA TTTCCGACGG CGGAAATTGG ATTATCAAAG
 Z2491 TATCGCGGCG AAGCCGGTTA CGCCATCGGC TACTCAGTA TTTCCGACGG CGGAAATTGG ATTATCAAAG
 H41 TATCTCGCGGCG AAGCCGGTTA TGCCATCGGC TACTCAAGCA TTTCCGACGG CGGAAATTGG ATTATCAAAG
 EG329 TATCGCGGCG AAGCCGGTTA CGCCATCGGC TACTCAGTA TTTCCGACGG CGGAAATTGG ATTATCAAAG
 PMC21 TATCGCGGCG AAGCCGGTTA CGCCATCGGC TACTCAGTA TTTCCGACGG CGGAAATTGG ATTATCAAAG
 EG327 TATCGCGGCG AAGCCGGTTA TGCCATCGGC TACTCAAGCA TTTCCGACGG CGGAAATTGG ATTATCAAAG
 Consensus TATC-CGGCG AAGCCGGTTA -GCCATCGGC TACTC-AG-A TITC-G-C-- -GG-AATTGG -TTATCAA-G
 C5

1751 1815
 H15 GCACGGCTTC CGGCAATTCTG CGGGGCCATT TCGGTGCTTC CGCATCTGTC GGTTATCAGT GGTAA
 BZ10 GCACGGCTTC CGGCAATTCTG CGGGGCCATT TCGGTACTTC CGCATCTGTC GGTTATCAGT GGTAA
 BZ198 GCACGGCTTC CGGCAATTCTG CGGGGCCATT TCGGTGCTTC CGCATCTGTC GGTTATCAGT GGTAA
 P20 GCACGGCTTC CGGCAATTCTG CGGGGCCATT TCGGTACTTC CGCATCTGTC GGTTATCAGT GGTAA
 H38 GCACGGCTTC CGGCAATTCTG CGGGGCCATT TCGGTGCTTC CGCATCTGTC GGTTATCAGT GGTAA
 Z2491 GCACGGCTTC CGGCAATTCTG CGGGGCCATT TCGGTGCTTC CGCATCTGTC GGTTATCAGT GGTAA
 H41 GCACGGCTTC CGGCAATTCTG CGGGGCCATT TCGGTGCTTC CGCATCTGTC GGTTATCAGT GGTAA
 EG329 GCACGGCTTC CGGCAATTCTG CGGGGCCATT TCGGTGCTTC CGCATCTGTC GGTTATCAGT GGTAA
 PMC21 GCACGGCTTC CGGCAATTCTG CGGGGCCATT TCGGTGCTTC CGCATCTGTC GGTTATCAGT GGTAA
 EG327 GCACGGCTTC CGGCAATTCTG CGGGGCCATT TCGGTGCTTC CGCATCTGTC GGTTATCAGT GGTAA
 Consensus GCACGGCTTC CGGCAATTCTG CGGGGCCATT TCGGT-CTTC CGCATCTGTC GGTTATCAGT GGTAA
 C5

FIG. 2 cont.

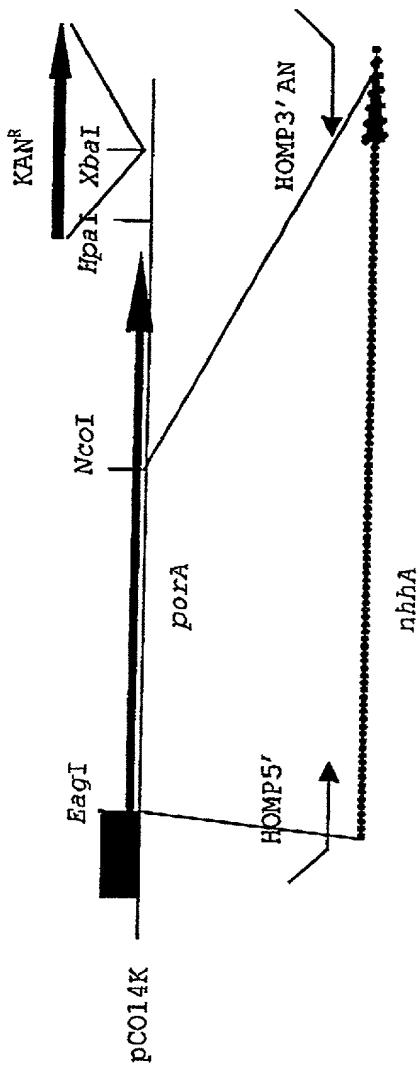


FIG. 3A

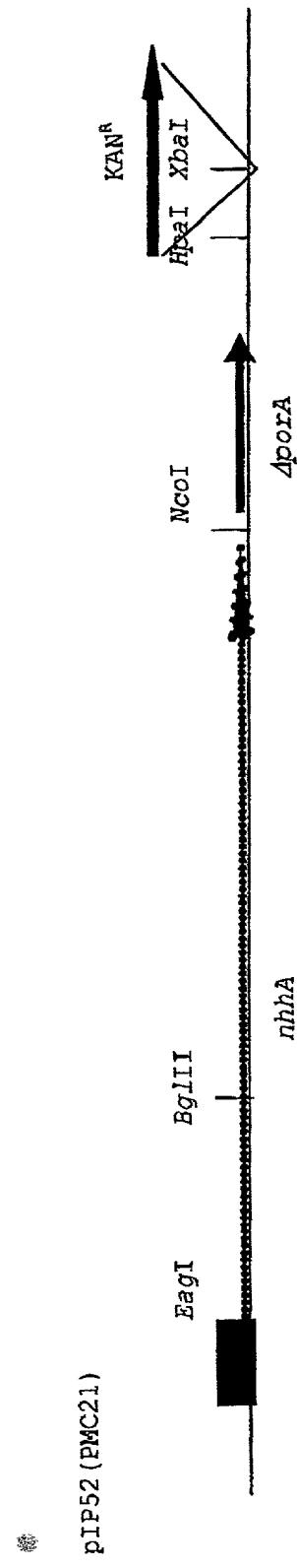


FIG. 3B

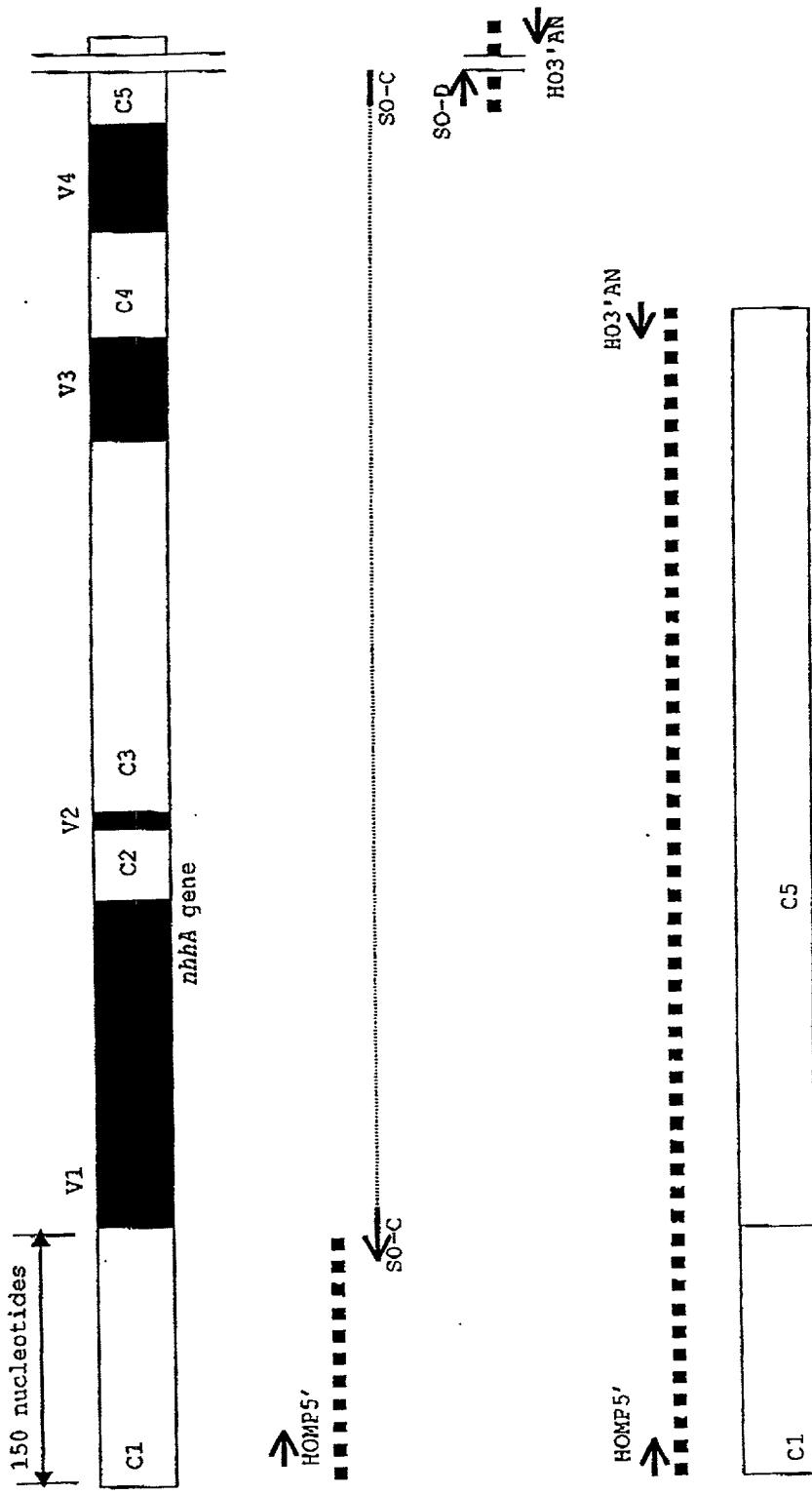


FIG. 4A

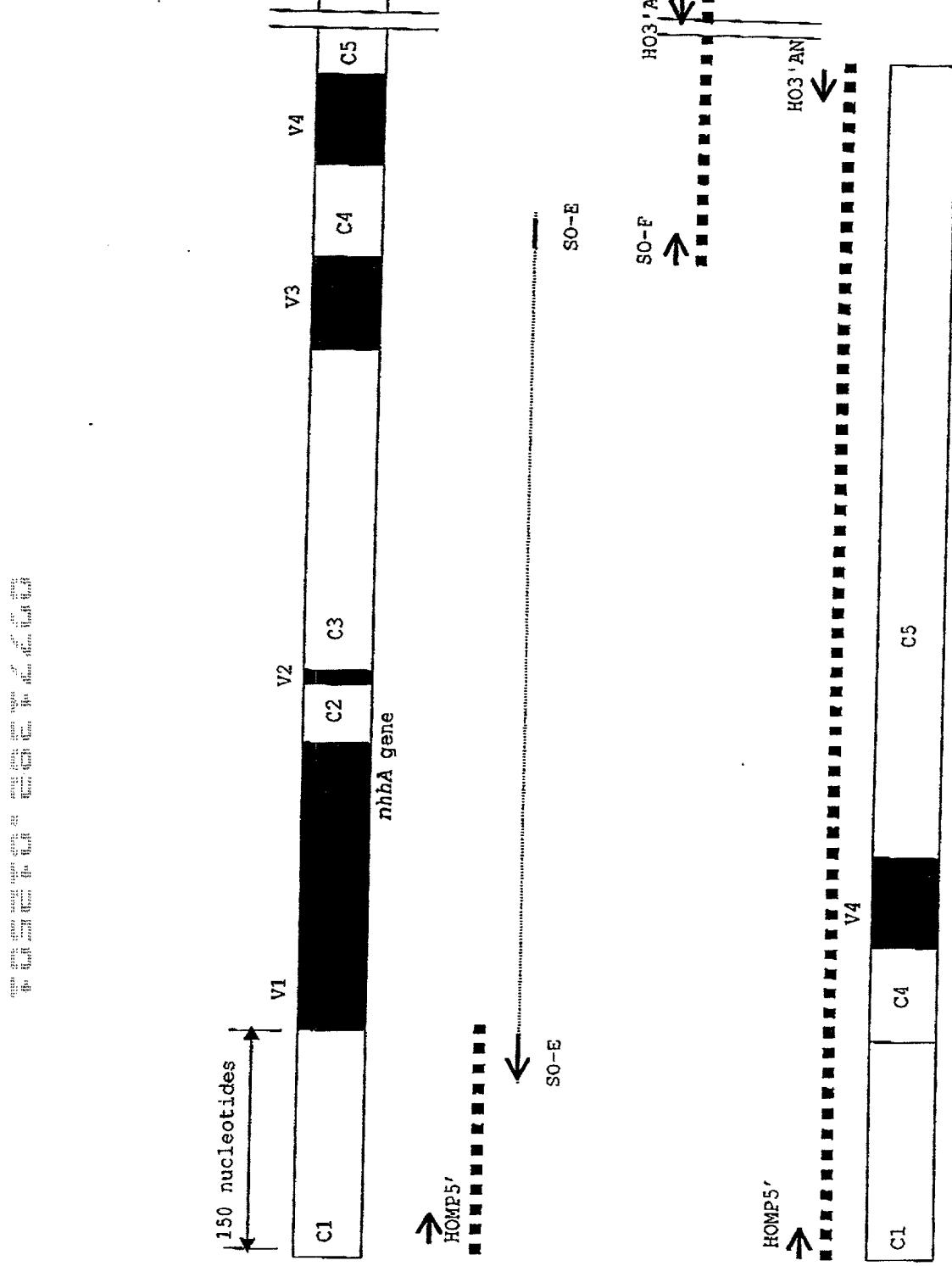


FIG. 4B

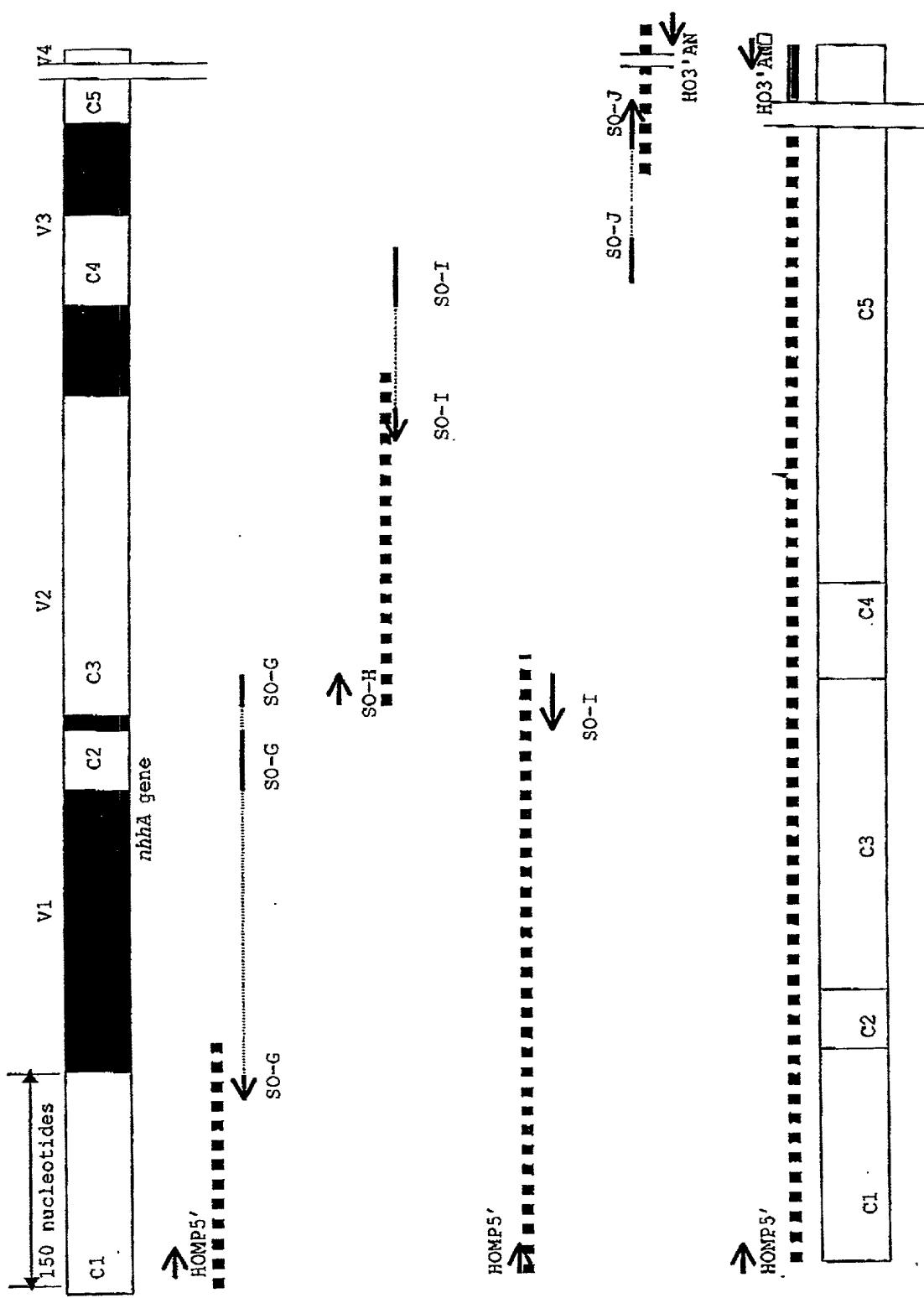


FIG. 4C

A

1 MNKIIYRIIWN SALNAWVVVS ELTRNHTKRA SATVKTAVLA TLLFATVQAS
 51 ANNETDLTSV GTEKLSFSAN GNKVNITSDE KGLNFAKETA GTNGDTTVHL
 101 NGIGSTLTDT LLNTGATTNV TNDNVTDDEK KRAASVKDVL NAGWNIGVK
 151 PGTTASDNVD FVRTYDTVEF LSADTKTTV NVESKDNGKK TEVKIGAKTS
 201 VIKEKGKLV TGKDKGENGS STDEGEGLVT AKEVIDAVNK AGWRMKTAA
 251 NGQTGQADKF ETVTSGTNVT EASGKGTAT VSKDDQGNIT VMYDVNVGDA
 301 LNVNQLQNSG WLDSKAVAG SSGKVISGNV SPSKGKMDT VNINAGNNIE
 351 ITRNGKNIDI ATSMTPQFSS VSLGAGADAP TLSVDGDALN VGSKKDNKPV
 401 RITNVAPGVK EGDVTNVAQL KGVAQNLNNR IDNVDGNARA GIAQAIATAG
 451 LVQAYLPGKS MMAIGGGTYR GEAGYAIGYS SISDGGNWII KGTASGNSRG
 501 HFGASASVGY QW*

B

1 ATGAACAAAA TATACCGCAT CAFTTCCAAT AGTGCCTCA ATGCATGGGT
 51 CGTCGTATCC GAGCTCACAC GCAACCACAC CAAACCGGCC TCCGCAACCG
 101 TGAAGACCGC CGTATTGGCG ACTCTGTTG TTGCAACGGT TCAGGCAAGT
 151 GCTAACAAATG AAACAGATCT GACCAAGTGT GGAACGTAAA AATTATCGTT
 201 TAGCGCAAAC GGCAATAAAG TCAACATCAC AAGCGACACC AAAGGCTTGA
 251 ATTTTGCGAA AGAAACGGCT GGGACGAACG GCGACACCCAC GGTCATCTG
 301 AACGGTATTG GTTCGACTTT GACCGATAACG CTGCTGAATA CCGGAGCGAC
 351 CACAAACGTA ACCAACGACA ACGTTACCGA TGACGAGAAA AAACGTGCGG
 401 CAAGCGTTAA AGACGTATTAA AACGCTGGCT GGAACATTAA AGGCCTTAAA
 451 CCCGGTACAA CAGCTTCCGA TAACGTTGAT TTCGTCGGCA CTTACGACAC
 501 AGTCGAGTTC TTGAGCGCAG ATACGAAAAC AACGACTCTT AATGTGGAAA
 551 GCAAAGACAA CGGCAAGAAA ACCGAAGTTA AAATCGGTGC GAAGACTTCT
 601 GTTATTAAAG AAAAGAGACGG TAAGTTGGCT ACTGGTAAAG ACAAAGGCGA
 651 GAATGGTTCT TCTACAGACG AAGGGCAAGG CTTAGTGAAT GCAAAAGAAG
 701 TGATTGATGC AGTAAACAAAG GCTGGTTGGG GAATGAAAAC AACAAACCGCT
 751 AATGGTCAAA CAGGTCAAGC TGACAAAGTTT GAAACCGTTA CATCAGGCAC
 801 AAATGTAACC TTTGCTAGTG GTAAAGGTAC AACTGCGACT GTAAAGTAAAG
 851 ATGATCAAGG CAACATCACT GTTATGTATG ATGTAATGT CGGGGATGCC
 901 CTAAACGTCA ATCAGCTGCA AAACAGCGGT TGGAAATTGG ATTCCAAAGC
 951 GGTTGCAGGT TCTTCGGGCA AAGTCATCAG CGGCAATGTT TCGGGGAGCA
 1001 AGGGAAAGAT GGATGAAACC GTCAACATTA ATGCCGGCAA CAACATCGAG
 1051 ATTACCGCA ACGGTAAAAA TATCGACATC GCCACTTCGA TGACCCCGCA
 1101 GTTTTCCAGC GTTTCGCTCG GCGGGGGGC GGATGCGCCC ACTTTGAGCG
 1151 TGGATGGGGGA CGCATTGAAT GTCGGCAGCA AGAAGGACAA CAAACCCGTC
 1201 CGCATTACCA ATGTCGCCCG GGGCGTTAAA GAGGGGGATG TTACAAACGT
 1251 CGCACAACCTT AAAGGGCGTGG CGCAAAACCTT GAACAACCGC ATCGACAATG
 1301 TGGACGGCAA CGCGCGTGGC GGCATCGCCC AAGCGATTGC AACCCGAGGT
 1351 CTGGTTCAAGG CGTATTGTC CCGCAAGAGT ATGATGGCGA TCGGGCGCGG
 1401 CACTTATCGC GGCGAAGCCG GTTACGCCAT CGGCTACTCC AGTATTTCGG
 1451 ACGGCGGAAA TTGGATTATC AAAGGCACGG CTTCCGGCAA TTCGGCGCGC
 1501 CATTTCGGTG CTTCCGCATC TGTGGTTAT CAGTGGTAA

FIG. 5

1 MNKIYRIIWN SALNAWVAVS ELTRNHTKRA SATVKTAVLA TLLFATVQAN
 51 ATDETGLINV ETEKLSFGAN GKKVNIISDT KGLNFAKETA GTNGDTTVHL
 101 NGIGSTLTDN LLNTGATTNV TNDNVTDDEK KRAASVKDVL NAGWNIKGVK
 151 PGTTASDNVD FVRTYDTVEF LSADTKTTTV NVESKDNGKK TEVKIGAKTS
 201 VIKEKDGGKLV TGKGKGENGSS STDEGEGLVT AKEVIDAVNK AGWRMKT
 251 NGQTGQADKF ETVTSGTKVT FASNGTTAT VSKDDQGNIT VKYDVNVGDA
 301 LNVNQLQNSG WNLDLSKAVAG SSGKVISGNV SPSKGKMDT VNINAGNNIE
 351 ITRNGKNIDI ATSMTPQFSS VSLGAGADAP TLSVDDEGAL NVGSKDANKP
 401 VRITNVAPGV KEGDVTNVAQ LKGVAQNLNN RIDNVNGNAR AGIAQAIATA
 451 GLVQAYLPKG SMMAIGGGTY LGEAGYAIGY SSISAGGNWI IKGTASGNSR
 501 GHFGASASVG YQW*

A

1 ATGAACAAAA TATACCGCAT CATTGGAAT AGTGCCTCA ATGCCTGGGT
 51 CGCCGTATCC GAGCTCACAC GCAACCACAC CAAACGCCGC TCCGCAACCG
 101 TGAACACCGC CGTATTGGCG ACACTGTTGT TTGCAACGGT TCAGGGGAAT
 151 GCTACCGATG AACACAGGCCT GATCAATGTT GAAACTGAAA AATTATCGTT
 201 TGGCCAAAC GGCAGAAG TCAACATCAT AAGGCACACC AAAGGCTTGA
 251 ATTCGCGAA AGAAAACGGCT GGGACGAACG GCACACCCAC GGTTCATCTG
 301 AACGGTATCG GTTCGACTTT GACCGATATG CTGCTGAATA CCGGAGCGAC
 351 CACAAACGTA ACCAACGACA ACGTTACCGA TGACGAGAAA AAACGTGCGG
 401 CAAGCGTTAA AGACGTATTA AACGCAGGCT GGAACATTAA AGGCCTTAAA
 451 CCCGGTACAA CAGCTTCCGA TAACGTGAT TTCTGCTCCGCA CTTACGACAC
 501 AGTCGAGTTC TTGAGCGCAG ATACGAAAAC AACGACTGTT AATGTGGAAA
 551 GCAAAGACAA CGGCAAGAAA ACCGAAGTTA AAATCGGTGC GAAGACTTCT
 601 GTTATTAAAG AAAAGACGG TAAGTTGGTT ACTGGTAAAG GCAAAGGCGA
 651 GAATGGTTCT TCTACAGACCC AAGGCGAAGG CTTAGTGACT GCAAAGAAG
 701 TGATTGATGC AGTAAACAAAG GCTGGTTGGA GAATGAAAAC AACAAACCGCT
 751 AATGGTCAAA CAGGTCAAGC TGACAAGTTT GAAACCGTTA CATCAGGCAC
 801 AAAAGTAACC TTGCTAGTG GTAATGGTAC AACTGCGACT GTAAGTAAAG
 851 ATGATCAAGG CAACATCACT GTTAAGTATG ATGTAATGT CGGCATGCC
 901 CTAAACGTCA ATCAGCTGCA AAACAGCGGT TCCAATTGG ATTCAAAGC
 951 GGTTGCAGGT TCTTCGGGCA AAGTCATCAG CGCAATGTT TCGCCGAGCA
 1001 AGGGAAAGAT GGATGAAACC GTCAACATTA ATGCCGGCAAAACATCGAG
 1051 ATTACCCGCA ACGGCAAAAA TATCGACATC GCCACTTCGA TGACCCGCA
 1101 ATTTTCAGC GTTTCGCTCG GCGCGGGGGC GGATGCGCCC ACTTTAACCG
 1151 TGGATGACGA GGGCGCGTT AATGTCGGCA GCAAGGATGC CAACAAACCC
 1201 GTCCGCATTA CCAATGTCGC CCCGGCGTT AAAGAGGGGG ATGTTACAAA
 1251 CGTCGCGCAA CTAAAGGTG TGGCGCAAAA CTGAAACAAAC CGCATCGACA
 1301 ATGTGAACGG CAACGCGCGT GCGGGCATCG CCCAAGCGAT TGCAACCGCA
 1351 GGTCTGGTTC AGGCCTATCT GCCCGGCAAG AGTATGATGG CGATCGGCGG
 1401 CGGCACCTTAT CTCGGCGAAG CCGGTTATGC CATCGGCTAC TCAAGCATT
 1451 CCGCCGGCGG AAATTGGATT ATCAAAGGCA CGGCTTCCGG CAATTGCGC
 1501 GGCCATTTCG GTGCTTCCGC ATCTGTCGGT TATCAGTGGT AA

B

FIG. 6

1 MNKIIYRIIWN SALNAWVVVS ELTRNHTKRA SATVKTAVLA TLLFATVQAS
51 ANNVDVFRTY DTVEFLSADT KTTTVNVESK DNGKKTEVKI GAKTSVIKEK
101 DGKLVTGKDK GENGSSTDEG EGLVLTAKEV DAVNKAGWRM KTTTANGQTG
151 QADKFETVTS GTNVTFAASGK GTTATVSKDD QGNITVMYDV NVGDALNVNQ
201 LQNSGWNLDS KAVAGSSGKV ISGNVSPSKG KMDETVNINA GNNIEITRNG
251 KNIDIATSMY PQFSSVSLGA GADAPTLSVD GDALNVGSKK DNKPVRITNV
301 APGVKEGDVT NVAQLKGVAQ NLNNRIDNVD GNARAGIAQA IATAGIVQAY
351 LPGKSMMIAIG GGTYRGEAGY AIGYSSISDG GNWIICKTAS GNSRGHFGAS
401 ASVGYQW*

A

1 ATGAAACAAA TATACCGCAT CATTGGAAT AGTGCCCTCA ATGCATGGGT
51 CGTCGTATCC GAGCTCACAC GCAACCACAC CAAACGCC TCCGCAACCG
101 TGAAGACCGC CGTATTGGCG ACTCTGTTGT TTGCAACCGGT TCAGGCAAGT
151 GCTAACAAACG TTGATTTCGT CCGCACTTAC GACACAGTCG AGTTCTTGAG
201 CGCAGATAACG AAAACAACGA CTGTTAATGT GGAAAGCAAA GACAACGGCA
251 AGAAAACCGA AGTTAAAATC GGTGCGAAGA CTTCTGTTAT TAAAGAAAAAA
301 GACGGTAAGT TGGTTACTGG TAAAGACAAA GGCGAGAATG GTTCTTCTAC
351 AGACGAAGGC GAAGGCTTAG TGACTGCAAAGAAGTGATT GATGCAGTAA
401 ACAAGGCTGG TTGGAGAATG AAAACAACAA CCGCTAATGG TCAACACAGT
451 CAAGCTGACA AGTTTGAAC CGTTACATCA GGCACAAATG TAACCTTTGC
501 TAGTGGTAAA GGTACAACTG CGACTGTAAG TAAAGATGAT CAAGGCAACA
551 TCACTGTTAT GTATGATGTA AATGTCGGCG ATGCCCTAAA CGTCAATCAG
601 CTGCAAAACA CGGGTTGGAA TTTGGATTCC AAAGCGGTTG CAGGTTCTTC
651 GGGAAAGTC ATCAGCGGCA ATGTTCGCC GAGCAAGGGAA AAGATGGATG
701 AAACCGTCAA CATTAAATGCC GGCAACAACA TCGAGATTAC CCGCAACGGT
751 AAAAATATCG ACATCGCCAC TTCGATGACC CCGCAGTTT CCAGCGTTTC
801 GCTCGCGCG GGGCGGGATG CGCCCACTTT GAGCGTGGAT GGGGACGCAT
851 TGAATGTCGG CAGCAAGAAG GACAACAAAC CCGTCCGCAT TACCAATGTC
901 GCCCCGGCG TTAAAGAGGG GGATGTTACA AACGTCGCAC AACTTAAAGG
951 CGTGGCGCAA AACTTGAACA ACCGCATCGA CAATGTGGAC GGCAACGCAC
1001 GTGCGGGCAT CGCCCAAGCG ATTGCAACCG CAGGTCTGGT TCAGGCGTAT
1051 TTGCCCGGCA AGAGTATGAT GGCGATCGGC GGCAGGCACTT ATCGCGGCGA
1101 AGCCGGTTAC GCCATCGGCT ACTCCAGTAT TTCCGACGGC GGAAATTGGA
1151 TTATCAAAGG CACGGCTTCC GGCAATTCCG GCGGCCATT CGGTGCTTCC
1201 GCATCTGTCG GTTATCAGTG GTAA

B

FIG. 7

1 MNKIVRIIWN SALNAWVVVS ELTRNHTKRA SATVKTAVLA TLLFATVQAS
 51 ANRAASVKDV LNAGWNIKGV KPGTTASDNV DFVRTYDTVE FLSADTKTTT
 101 VNVESKDNGK KTEVKIGAKT SVIKEKDGL VTKDKDGENG SSTDEGEGLV
 151 TAKEVIDAVN KAGWRMKTTT ANGQTGQADK FETVTSGTNV TFASGKGTTA
 201 TVSKDDQGNI TVMYDVNVGD ALNVNQLQNS GWNLDSKAVA GSSGKVISGN
 251 VSPSKGKMD EITRNGKNID IATSMTPOFS SVSLGAGADA
 301 PTLSVVDGDAL NVGSKKDNKP VRITNVAPGV KEGDVTNVAQ LKGVAQNLNN
 351 RIDNVDGNAR AGIAQAIATA GLVQAYLPGK SMMAIGGGTY RGEAGYAIGY
 401 SSISDGNNWI IKGTASGNSR GHFGASASVG YQW*

A

1 ATGAACAAAA TATACCGCAT CATTGGAAT AGTGCCTCA ATGCATGGGT
 51 CGTCGTATCC GAGCTCACAC GCAACCACAC CAAACGCGCC TCCGCAACCG
 101 TGAAGACCGC CGTATTGGCG ACTCTGTTGT TTGCAACGGT TCAGGCAAGT
 151 GCTAACCGTG CGGCAAGCGT TAAAGACGTA TAAACGCTG GCTGGAACAT
 201 TAAAGGCCTT AAACCCGGTA CAACAGCTTC CGATAACGTT GATTTCGTCC
 251 GCACTTACGA CACAGTCGAG TTCTTGAGCG CAGATACGAA AACAAAGACT
 301 GTTAATGTGG AAAGCAAAGA CAACGGCAAG AAAACCGAAG TTAAAATCGG
 351 TGCAGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA
 401 AAGACAAGG CGAGAATGGT TCTTCTACAG ACCAAGGCAG AGGCTTAGTG
 451 ACTGCAAAG AAGTGATTGA TGCAGTAAAC AAGGCTGGTT GGAGAATGAA
 501 ACAACAAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG TTTGAAACCG
 551 TTACATCAGG CACAAATGTA ACCTTTGCTA GTGGTAAAGG TACAACGTGCG
 601 ACTGTAAGTA AAGATGATCA AGGCAACATC ACTGTTATGT ATGATGTAAA
 651 TGTCGGCGAT GCCTCTAAACG TCAATCAGCT GCAAAACAGC GGTTGGAATT
 701 TGGATTCCAA AGCGGTTGCA GGTTCTTCGG GCAAAGTCAT CAGCGGCAAT
 751 GTTTCGCCGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCGG
 801 CAAACAACATC GAGATTACCC GCAACGGTAA AAATATCGAC ATCGCCACTT
 851 CGATGACCCC GCAGTTTCGC AGCGTTTCGC TCGGCGCGGG GGCGGATGCG
 901 CCCACTTGA GCGTGGATGG GGACGCATTG AATGTCGGCA GCAAGAAGGA
 951 CAAACAAACCC GTCCGCATTA CCAATGTCGC CCCGGCGTT AAAGAGGGGG
 1001 ATGTTACAAA CGTCGCACAA CTTAAAGGCG TGGCGAAAA CTTGAACAAAC
 1051 CGCATCGACA ATGTTGACGG CAACCGCGT GCGGGCATCG CCCAAGCCGAT
 1101 TGCAACCGCA GGTCTGGTTC AGGCGTATTT GCCCGGCAAG AGTATGATGG
 1151 CGATCGGCAG CGGCACATTAT CGCGGCGAAG CCGGTTACGC CATCGGCTAC
 1201 TCCAGTATTT CCAGACGGCGG AAATTGGATT ATCAAAGGCA CGGCTTCCGG
 1251 CAATTGCGC GGCCATTTCG GTGCTTCCGC ATCTGTCGGT TATCAGTGGT
 1301 AA

B

FIG. 8

1 MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVKTAVLA TLLFATVQAS
 51 ANTLKAGDNL KIKQFTYSLK KDLTDLTSVG TEKLSFSANG NKVNITSDTK
 101 GLNFAKETAG TNGDTTVHLN GIGSTLTDRA ASVKDVLMAG WNIKGVKNVD
 151 FVRTYDTVEF LSADTKTTTV NVESKDNGKK TEVKIGAKTS VIKEKDGLV
 201 TGDKGENGS STDEGEGLVT AKEVIDAVNK AGWRMKTGTTA NGOTQADKE
 251 ETVTSGTNVT FASGKGTTAT VSKDDQGNIT VMYDVNVGDA LNVNQLQNSG
 301 WNLDSSKAVAG SSGKVISGNV SPSKGKMDT VNINAGNNIE ITRNGKNIDI
 351 ATSMTPQFSS VSLGAGADAP TLSVGDALN VGSKKDNKPV RITNVAPGVK
 401 EGDVTNVAQL KGVAQNLNNR IDNVDGNARA GLAQAIATAG LVQAYLPGKS
 451 MMAIGGGTYR GEAGYAIGYS SISDGGNWII KGTASGNSRG HFGASASVGY
 501 QW*

A

1 ATGAACAAAA TATAACCGCAT CATTGGAAT AGTGCCCTCA ATGCATGGGT
 51 CGTCGTATCC GAGCTCACAC GCAACCACAC CAAACGCGCC TCCGCAACCG
 101 TGAAGACCGC CGTATTGGCG ACTCTGTTGT TTGCAACGGT TCAGGCAAGT
 151 GCTAACACCCC TCAAAGCCGG CGACAACCTG AAAATCAAAC AATTCACCTA
 201 CTCGCTGAAA AAAGACCTCA CAGATCTGAC CAGTGTGGA ACTGAAAAAT
 251 TATCGTTTAG CGCAAAACGGC AATAAAGTCA ACATCACAAG CGACACCAAA
 301 GGCTTGAATT TTGCGAAAGA AACGGCTGGG ACGAACGGCG ACACCAACGGT
 351 TCATCTGAAC GGTATTGGTT CGACTTTGAC CGATCGTGCG GCAAGCGTTA
 401 AAGACGTATT AAACGCTGGC TGGAACATTA AAGGCCTTAA AACACGTGAT
 451 TTCGTCCGCA CTTACGACAC AGTCGAGTTC TTGAGCQCAG ATACGAAAAC
 501 AACGACTGTT AATGTGAAAG GCAAAGACAA CGGCAAGAAA ACCGAAGTTA
 551 AAATCGGTGC GAAGACTTCT GTTATTAAAG AAAAAGACGG TAAGTTGGTT
 601 ACTGGTAAAG ACAAAAGCGA GAATGGTTCT TCTACAGACG AAGGCAGG
 651 CTTAGTGACT GCAAAAGAAG TGATTGATGC AGTAAACAAAG GCTGGTTGG
 701 GAATGAAAAC AACAAACCGCT AATGGTCAAA CAGGTCAAGC TGACAAGTTT
 751 GAAACCGTTA CATCAGGCAC AAATGTAACC TTGCTAGTG GTAAAGGTAC
 801 AACTGCGACT GTAAGTAAAG ATGATCAAGG CAACATCACT GTTATGTATG
 851 ATGTAATGT CGGCGATGCC CTAAACGTCA ATCAGCTGCA AAACAGCGGT
 901 TGGAAATTGG ATTCCAAAGC GGTGTCAGGT TCTTCGGCA AAGTCATCAG
 951 CGGCAATGTT TCGCCGAGCA AGGGAAAGAT GGATGAAACC GTCAACATTA
 1001 ATGCCGGCAA CAACATCGAG ATTACCCGCA ACGGTAAGAA TATCGACATC
 1051 GCCACTTCGA TGACCCCCCA GTTTTCCAGC GTTTCGCTCG GCGCGGGGGC
 1101 GGATGCGCCC ACTTTGAGCG TGGAATGGGGCA CGCATTGAAAT GTCGGCAGCA
 1151 AGAAGGACAA CAAACCCGTC CGCATTACCA ATGTCGCCCG GGGCGTTAAA
 1201 GAGGGGGATG TTACAAAACGT CGCACAACTT AAAGGCCTGG CGCAAAACTT
 1251 GAACAACCGC ATCGACAATG TGGACGGCAA CGCGCGTGC GGCATCGCCC
 1301 AAGCGATTGC AACCGCAGGT CTGGTTCAAG CGTATTGCC CGGCAAGAGT
 1351 ATGATGGCGA TCGGGGGCGG CACTTATGCC GGCGAAGCCG GTTACGCCAT
 1401 CGGCTACTCC AGTATTTCGG ACGGCGGAAA TTGGATTATC AAAGGCACGG
 1451 CTTCCGGCAA TTTCGCGCGGC CATTTCGGTG CTTCCGCATC TGTCGGTTAT
 1501 CAGTGGTAA

B

FIG. 9

				1
H41	MNKIYRIIWN SALNAWAVS ELTRNHTKRA SATVKTAVLA TLLFATVQAN			
PMC21	MNKIYRIIWN SALNAWVVVS DLTRNHTKRA SATVNTAVLA TLLFATVQAS			
H41Studel	MNKIYRIIWN SALNAWAVS ELTRNHTKRA SATVKTAVLA TLLFATVQAN			
PMC21Bglde1	MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVKTAVLA TLLFATVQAS			
PMC21C1C5	MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVKTAVLA TLLFATVQAS			
	C1			
	51			
H41	ATDED...EEE ELESVQRS.V VGSIOASMEG SVELET...I SLSMTNDOSKE			100
PMC21	ANNEEQEEYL YLHPVQRTVA VLIVNSDKEG AGEKEKVEEN SDWAVYFNEK			
H41Studel	ATDE...			
PMC21Bglde1	ANNE...			
PMC21C1C5	AN ...			
	V1			
	101			
H41	FVDPYIVVTL KAGDNLKIKO N.TNENTNAS SFTYSILKKDL TGLINVETE			150
PMC21	GVLTAREITL KAGDNLKIKO NGTN FTYSILKKDL TDLTSGTEK			
H41Studel			
PMC21Bglde1			
PMC21C1C5			
	V1	C2	V2	C3
	151			
H41	LSFGANGKKV NIISDTKGLN FAKETAGTNG DTTVHLNGIG STLTDMILLNT			200
PMC21	LSFSAHGNKV NITSDTKGLN FAKETAGTNG DTTVHLNGIG STLTDTLLNT			
H41Studel	LSFGANGKKV NIISDTKGLN FAKETAGTNG DTTVHLNGIG STLTDMILLNT			
PMC21Bglde1	LSFSANGNKV NITSDTKGLN FAKETAGTNG DTTVHLNGIG STLTDTLLNT			
PMC21C1C5			
	C3			V3
	201			
H41	GATTNVTNDN VTDEDEKKRAA SVKDVLNAGW NIKGVKPGTT ASDNVDFVRT			250
PMC21	GATTNVTNDN VTDEDEKKRAA SVKDVLNAGW NIKGVKPGTT ASDNVDFVRT			
H41Studel	GATTNVTNDN VTDEDEKKRAA SVKDVLNAGW NIKGVKPGTT ASDNVDFVRT			
PMC21Bglde1	GATTNVTNDN VTDEDEKKRAA SVKDVLNAGW NIKGVKPGTT ASDNVDFVRT			
PMC21C1C5			NVDFVRT
	V3		C4	V4
	251			C5
H41	YDTVEFLSAD TKTTTVNVES KDNGKKTEVK IGAKTSVIKE KDGKLVTGKG			300
PMC21	YDTVEFLSAD TKTTTVNVES KDNGKKTEVK IGAKTSVIKE KDGKLVTGKD			
H41Studel	YDTVEFLSAD TKTTTVNVES KDNGKKTEVK IGAKTSVIKE KDGKLVTGKG			
PMC21Bglde1	YDTVEFLSAD TKTTTVNVES KDNGKKTEVK IGAKTSVIKE KDGKLVTGKD			
PMC21C1C5	YDTVEFLSAD TKTTTVNVES KDNGKKTEVK IGAKTSVIKE KDGKLVTGKD			
	C5			
	301			
H41	KGENGSSTDE GEGLVTAKEV IDAVNKAGWR MKTTTANGQT QDAKFKETVT			350
PMC21	KGENGSSTDE GEGLVTAKEV IDAVNKAGWR MKTTTANGQT QDAKFKETVT			
H41Studel	KGENGSSTDE GEGLVTAKEV IDAVNKAGWR MKTTTANGQT QDAKFKETVT			
PMC21Bglde1	KGENGSSTDE GEGLVTAKEV IDAVNKAGWR MKTTTANGQT QDAKFKETVT			
PMC21C1C5	KGENGSSTDE GEGLVTAKEV IDAVNKAGWR MKTTTANGQT QDAKFKETVT			
	C5			
	351			
H41	SGTKVTFASG NGTTATVSKD DOGNITVKYD VNVDALNVN OLQNSGWNL			400
PMC21	SGTNVTFAASG KGTTATVSKD DOGNITVYMD VNVDALNVN OLQNSGWNL			
H41Studel	SGTKVTFASG NGTTATVSKD DOGNITVKYD VNVDALNVN OLQNSGWNL			
PMC21Bglde1	SGTNVTFAASG KGTTATVSKD DOGNITVYMD VNVDALNVN OLQNSGWNL			
PMC21C1C5	SGTNVTFAASG KGTTATVSKD DOGNITVYMD VNVDALNVN OLQNSGWNL			
	C5			

FIG. 10

		401	
H41	<u>SKAVAGSSGK</u>	<u>VISGNVSPSK</u>	<u>GKMDETVNIN</u>
PMC21	<u>SKAVAGSSGK</u>	<u>VISGNVSPSK</u>	<u>GKMDETVNIN</u>
H41Studel	<u>SKAVAGSSGK</u>	<u>VISGNVSPSK</u>	<u>GKMDETVNIN</u>
PMC21Bglde1	<u>SKAVAGSSGK</u>	<u>VISGNVSPSK</u>	<u>GKMDETVNIN</u>
PMC21C1C5	<u>SKAVAGSSGK</u>	<u>VISGNVSPSK</u>	<u>GKMDETVNIN</u>
		C5	
		451	
H41	<u>TPQFSSVSLG</u>	<u>AGADAPTLSV</u>	<u>DDEGALNVGS</u>
PMC21	<u>TPQFSSVSLG</u>	<u>AGADAPTLSV</u>	<u>KDANKPVRIT</u>
H41Studel	<u>TPQFSSVSLG</u>	<u>AGADAPTLSV</u>	<u>NVAPGVKEGD</u>
PMC21Bglde1	<u>TPQFSSVSLG</u>	<u>AGADAPTLSV</u>	<u>KKDNKPVRIT</u>
PMC21C1C5	<u>TPQFSSVSLG</u>	<u>AGADAPTLSV</u>	<u>NVAPGVKEGD</u>
		C5	
		501	
H41	<u>VTNVAQLKGV</u>	<u>AQNLNRRIDN</u>	<u>VNGNARAGIA</u>
PMC21	<u>VTNVAQLKGV</u>	<u>AQNLNRRIDN</u>	<u>QAIATAGLVO</u>
H41Studel	<u>VTNVAQLKGV</u>	<u>AQNLNRRIDN</u>	<u>AYLPGKSMMMA</u>
PMC21Bglde1	<u>VTNVAQLKGV</u>	<u>AQNLNRRIDN</u>	<u>VDGNARAGIA</u>
PMC21C1C5	<u>VTNVAQLKGV</u>	<u>AQNLNRRIDN</u>	<u>QAIATAGLVO</u>
		C5	
		551	
H41	<u>VTNVAQLKGV</u>	<u>AQNLNRRIDN</u>	<u>VNGNARAGIA</u>
PMC21	<u>VTNVAQLKGV</u>	<u>AQNLNRRIDN</u>	<u>QAIATAGLVO</u>
H41Studel	<u>VTNVAQLKGV</u>	<u>AQNLNRRIDN</u>	<u>AYLPGKSMMMA</u>
PMC21Bglde1	<u>VTNVAQLKGV</u>	<u>AQNLNRRIDN</u>	<u>VDGNARAGIA</u>
PMC21C1C5	<u>VTNVAQLKGV</u>	<u>AQNLNRRIDN</u>	<u>QAIATAGLVO</u>
		C5	
		601	
H41	<u>IGGGTYLGEA</u>	<u>GYAIGYSSIS</u>	<u>AGGNWIIKGT</u>
PMC21	<u>IGGGTYRGEA</u>	<u>GYAIGYSSIS</u>	<u>ASASVGYQW.</u>
H41Studel	<u>IGGGTYLGEA</u>	<u>GYAIGYSSIS</u>	<u>DGGNWIIKGT</u>
PMC21Bglde1	<u>IGGGTYRGEA</u>	<u>GYAIGYSSIS</u>	<u>ASGSNSRGHFG</u>
PMC21C1C5	<u>IGGGTYRGEA</u>	<u>GYAIGYSSIS</u>	<u>ASASVGYQW.</u>
		C5	

FIG. 10 cont'd

1 2 3 4 5 6

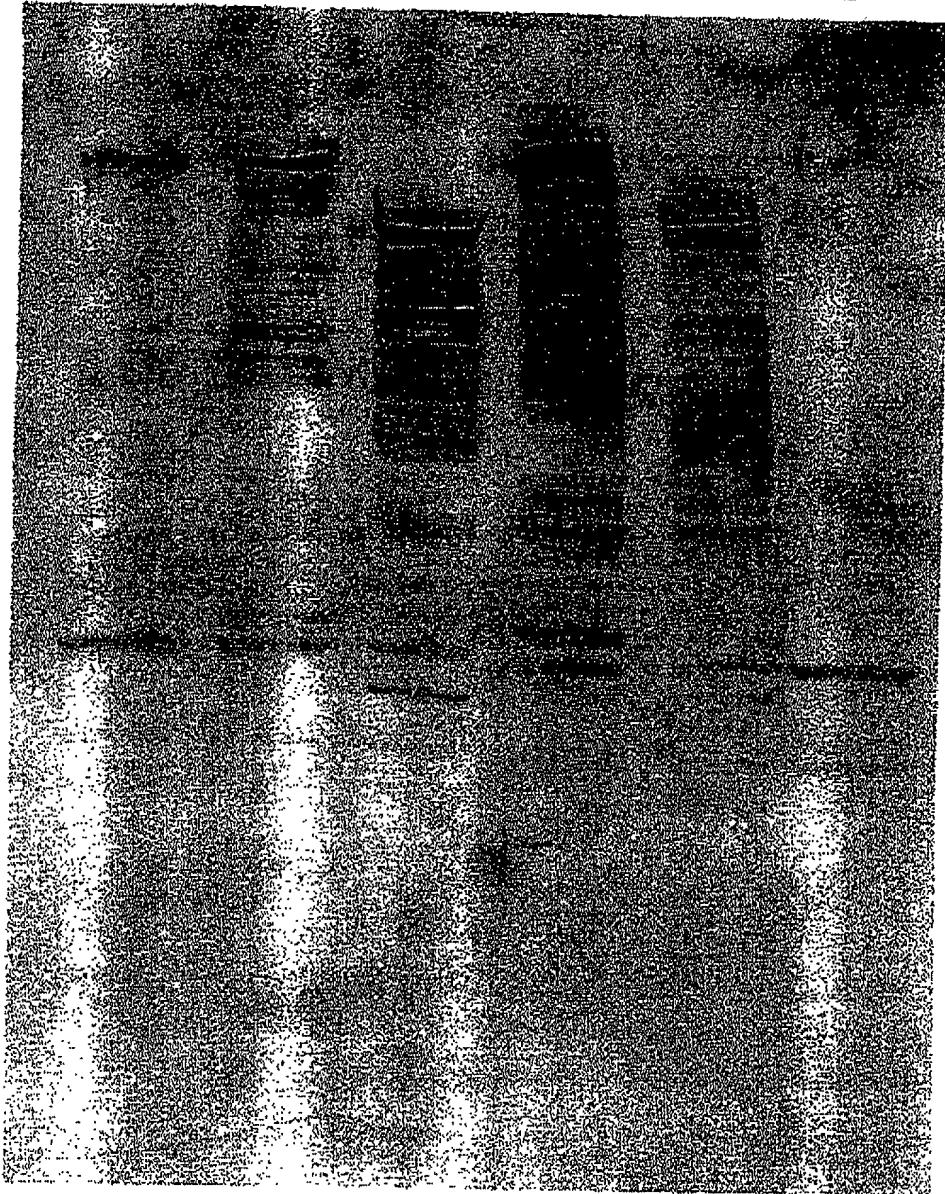


FIG. 11

1 2 3 4 5 6 7

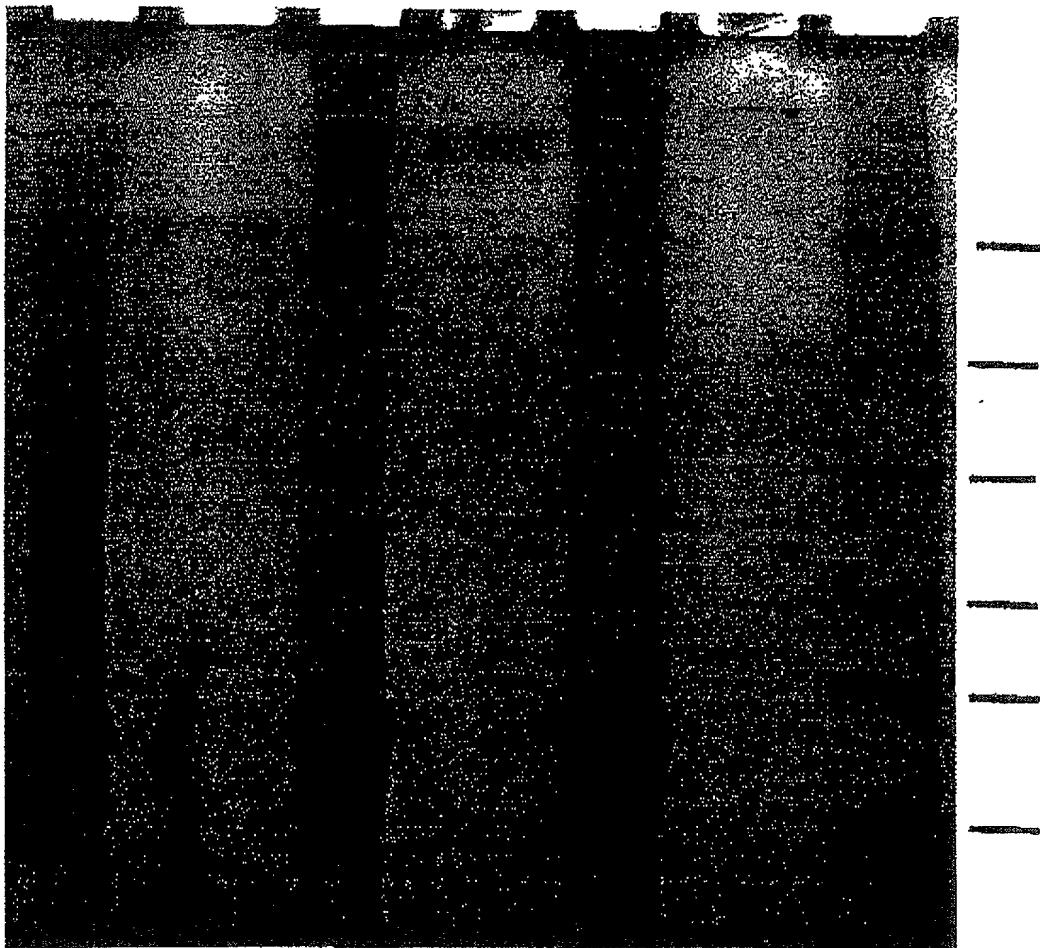
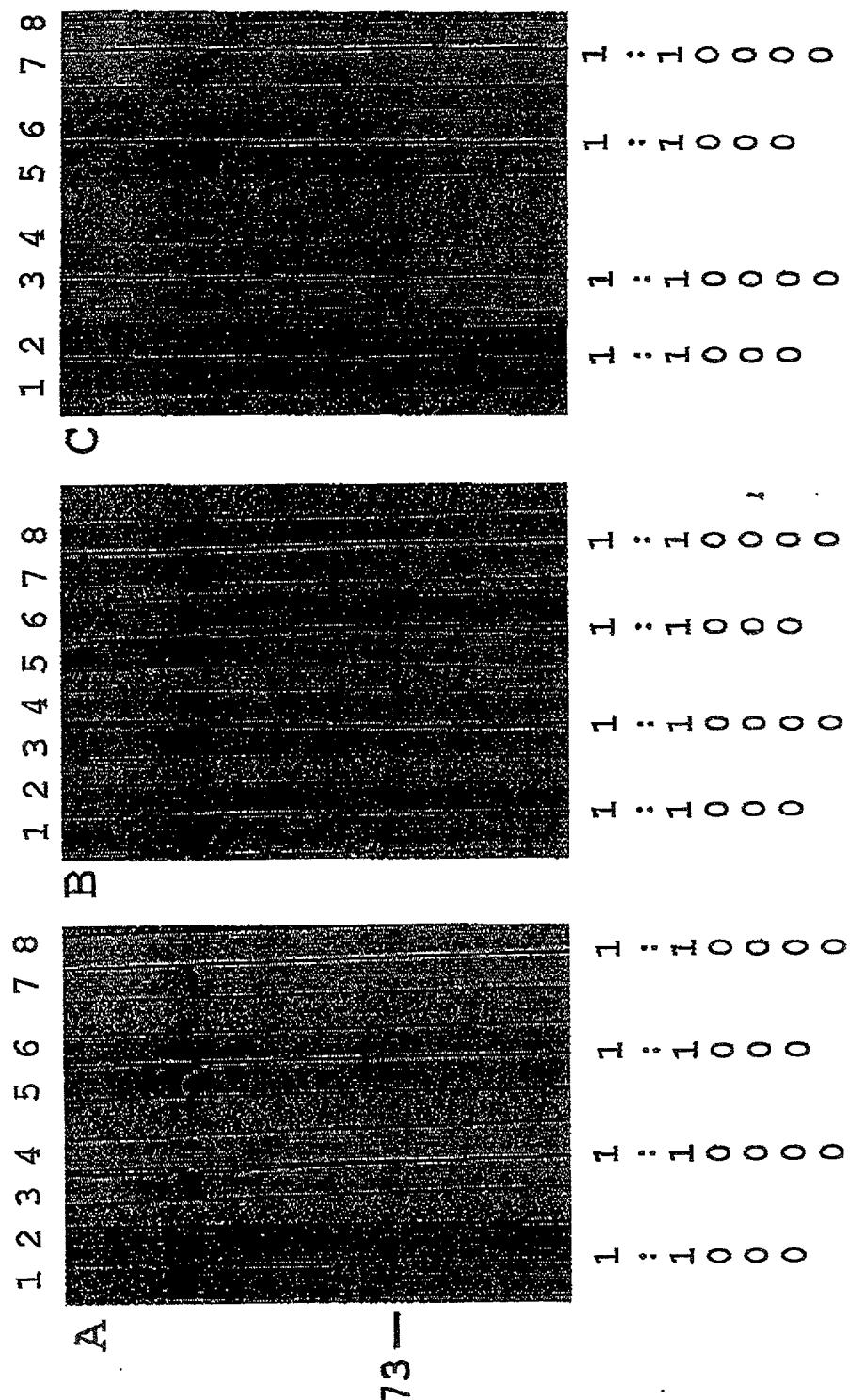


FIG. 12



173—

FIG. 13

A

52 NNEEQEEYL YLHPVQRTVA VLIVNSDKEG AGEKEKVEEN SDWAVYFNEK
101 GVLTAREITL KAGDNLKIKQ NGTNFTYSLK KDLTDLTSVG TEKLSFSAHG
151 NKVNITSDTK GLNFAKETAG TNGDTTVHLN GIGSTLTDL LNTGATTNVT
201 NDNVTDDEKK RAASVKDVLN AGWNIGVKP GTTASDNVDF VRTYDTVEFL
251 SADTKTTTVN VESKDNGKKT EVKIGAKTSV IKEKGKLVG GKDKGENGS
301 TDEGEGLVTA KEVIDAVNKA GWRMKTAN GQTGQADKFE TVTSGTNVT
351 ASGKGTTATV SKDDQGNITV MYDVNVGDAL NVNQLQNSGW NLDSKAVAGS
401 SGKVISGNVS PSKGKMDT V NINAGNNIEI TRNGKNIDIA TSMPQFSSV
451 SLGAGADAPT LSVDGDALNV GSKKDNKPVR ITNVAPGVKE GDVTNVAQLK
501 GVAQNLNNRI DNVDGNARAG IAQAIATAGL VQAYLPGKSM MAIGGGTYRG
551 EAGYAIGYSS ISDGGNWIIC GTASGNSRGH FGASASVGYQ W*

B

52 TDEDEEEEL ESVQRSVVGS IQASMEGSVE LETISLSMTN DSKEFVDPYI
101 VVTLKAGDNL KIKQNTNENT NASSFTYSLK KDLTGLINVE TEKLSFGANG
151 KKVNIIISDTK GLNFAKETAG TNGDTTVHLN GIGSTLTDML LNTGATTNVT
201 NDNVTDDEKK RAASVKDVLN AGWNIGVKP GTTASDNVDF VRTYDTVEFL
251 SADTKTTTVN VESKDNGKKT EVKIGAKTSV IKEKGKLVG GKDKGENGS
301 TDEGEGLVTA KEVIDAVNKA GWRMKTAN GQTGQADKFE TVTSGTKVTF
351 ASGNGTTATV SKDDQGNITV KYDVNVGDAL NVNQLQNSGW NLDSKAVAGS
401 SGKVISGNVS PSKGKMDT V NINAGNNIEI TRNGKNIDIA TSMPQFSSV
451 SLGAGADAPT LSVDDEGALN VGSKDANKPV RITNVAPGVK EGDVTNVAQL
501 KGVAQNLNNR IDNVNGNARA GIAQAIATAG LVQAYLPGKS MMAIGGGTYL
551 GEAGYAIGYS SISAGGNWII KGTASGNSRG HFGASASVGY QW*

FIG. 14

C

52 NNETDLTSV GTEKLSFSAN GNKVNITSDT KGLNFAKETA GTNGDTTVHL
101 NGIGSTLTD^T LLNTGATTNV TNDNVTDEK KRAASVKDVL NAGWNIKGVK
151 PGTTASDNVD FVRTYDTVEF LSADTKTTTV NVESKDNGKK TEVKIGAKTS
201 VIKEKDGGKL^V TGKDKGENGS STDEGEGLVT AKEVIDAVNK AGWRMKT^TTA
251 NGQTGQADKF ETVTSGTNVT FASGKGTTAT VSKDDQGNIT VMYDVNVGDA
301 LNVNQLQNSG WNLD^SSKAVAG SSGKVISGNV SPSKGKMD^ET VNINAGNNIE
351 ITRNGKNIDI ATSMTPQFSS VSLGAGADAP TLSVDGDALN VGSKKD^NKPV
401 RITNVAPGVK EGDVTNVAQL KGVAQNLNNR IDNVDGNARA GIAQAIATAG
451 LVQAYLPGKS MMAIGGGTYR GEAGYAIGYS SISDG^GGNWII KGTASGNSRG
501 HFGASASVG YQW*

D

52 TDETGLINV ETEKLSFGAN GKKVNIISDT KGLNFAKETA GTNGDTTVHL
101 NGIGSTLDM LLNTGATTNV TNDNVTDEK KRAASVKDVL NAGWNIKGVK
151 PGTTASDNVD FVRTYDTVEF LSADTKTTTV NVESKDNGKK TEVKIGAKTS
201 VIKEKDGGKL^V TGKKGGENGS STDEGEGLVT AKEVIDAVNK AGWRMKT^TTA
251 NGQTGQADKF ETVTSGTKVT FASGNGTTAT VSKDDQGNIT VKYDVNVGDA
301 LNVNQLQNSG WNLD^SSKAVAG SSGKVISGNV SPSKGKMD^ET VNINAGNNIE
351 ITRNGKNIDI ATSMTPQFSS VSLGAGADAP TLSVDDEGAL NVGSKDANKP
401 VRITNVAPGV KEGDVTNVAQ LKGVAQNLNN RIDNVNGNAR AGIAQAIATA
451 GLVQAYLPGK SMMAIGGGTY LGEAGYAIGY SSISAGGNWI IKGTASGNSR
501 GHFGASASVG YQW*

FIG. 14

E

52 NNVDFVRTY DTVEFLSA DT KTTTVNVESK DNGKKTEVKI GAKTSVIKEK
101 DGKLVTGDK GENGSSTDEG EGLVTAKEVI DAVNKAGWRM KTTTANGQTG
151 QADKFETVTS GTNVTFASGK GTTATVSKDD QGNITVMYDV NVGDALNVNQ
201 LQNSGWNLDS KAVAGSSGKV ISGNVSPSKG KMDETVNINA GNNIEITRNG
251 KNIDIATSM T PQFSSVSLGA GADAPTLSVD GDALNVGSKK DNKPVRITNV
301 APGVKEGDVT NVAQLKGVAQ NLNNRIDNVD GNARAGIAQA IATAGLVQAY
351 LPGKSMMAIG GGTYRGEAGY AIGYSSISDG GNWIIKGTAS GNSRGHFGAS
401 ASVGYQW*

F

52 NRAASVKDV LNAGWNIKGV KPGTTASDNV DFVRTYDTVE FLSADTKTTT
101 VNVESKDNGK KTEVKIGAKT SVIKEKDGL VTKDKGENG SSTDEGEGLV
151 TAKEVIDAVN KAGWRMKTTT ANGQTGQADK FETVTS GTNV TFASGKGTTA
201 TVSKDDQGNI TVMYDVNVGD ALNVNQLQNS GWNLDSKAVA GSSGKVISGN
251 VSPSKGKMDE TVNINAGNNI EITRNGKNID IATSMTPQFS SVSLGAGADA
301 PTLSVDGDAL NVGSKKDNKP VRITNVAPGV KEGDVTNVAQ LKGVAQNLNN
351 RIDNDVGNA AGIAQAIATA GLVQAYLPK SMMAIGGGTY RGEAGYAIGY
401 SSISDGGNWI IKGTASGNSR GHFGASASVG YQW*

G

50 SANTLKAGDNL KIKQFTYSLK KDLTDLTSG TEKLSFSANG NKVNITSDTK
101 GLNFAKETAG TNGDTTVHLN GIGSTLTDRA ASVKDVLNAG WNIKGVKNVD
151 FVRTYDTVEF LSADTKTTT VNESKDNGKK TEVKIGAKTS VIKEKDGLV
201 TGKDKGENGS STDEGEGLVT AKEVIDAVNK AGWRMKTTTA NGQTGQADKF
251 ETVTSGTNVT FASGKGTTAT VSKDDQGNIT VMYDVNVGDA LNVNQLQNSG
301 WNLD SKAVAG SSGKVISGNV SPSKGKMDT VNINAGNNIE ITRNGKNIDI
351 ATSMTPQFSS VSLGAGADAP TLSVDGDALN VGSKKDNKPV RITNVAPGVK
401 EGDVTNVAQL KGVAQNLNNR IDNDVGNA AGIAQAIATAG LVQAYLPK
451 MMAIGGGTYR GEAGYAIGYS SISDGGNWI KGTASGNSRG HFGASASVGY
501 QW*

FIG. 14